



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <b>C07H 21/04, C07K 14/705, C12N 15/09, 15/63, C12Q 1/68</b>		A1	(11) International Publication Number: <b>WO 99/57132</b>
			(43) International Publication Date: 11 November 1999 (11.11.99)
(21) International Application Number: PCT/US99/09970		(72) Inventors: JACOBS, Kenneth; 151 Beaumont Avenue, Newton, MA 02160 (US). McCOY, John, M.; 56 Howard Street, Reading, MA 01867 (US). LaVALLIE, Edward, R.; 113 Ann Lee Road, Harvard, MA 01451 (US). COLLINS-RACIE, Lisa, A.; 124 School Street, Acton, MA 01720 (US). EVANS, Cheryl; 18801 Bent Willow Circle, Germantown, MD 20874 (US). MERBERG, David; 2 Orchard Drive, Acton, MA 01720 (US). TREACY, Maurice; 12 Foxrock Court, Dublin 18 (IE). AGOSTINO, Michael, J.; 26 Wolcott Avenue, Andover, MA 01810 (US). STEININGER, Robert, J., II; 100 Reed Street, Cambridge, MA 02140 (US). BOWMAN, Michael, R.; 50 Aldrich Road, Canton, MA 02021 (US). DiBLASIO-SMITH, Elizabeth; 17 Chestnut Road, Tyngsboro, MA 01879 (US). WIDOM, Angela; 19 Cherokee Road, Acton, MA 01720 (US).	
(22) International Filing Date: 7 May 1999 (07.05.99)			
(30) Priority Data:			
60/084,564	7 May 1998 (07.05.98)	US	
60/087,645	2 June 1998 (02.06.98)	US	
60/093,712	22 July 1998 (22.07.98)	US	
60/094,935	31 July 1998 (31.07.98)	US	
60/095,880	10 August 1998 (10.08.98)	US	
60/096,068	11 August 1998 (11.08.98)	US	
Not furnished	6 May 1999 (06.05.99)	US	
(71) Applicant: GENETICS INSTITUTE, INC. [US/US]; 87 CambridgePark Drive, Cambridge, MA 02140 (US).		(74) Agent: MANDRAGOURAS, Amy, E.; Lahive & Cockfield, LLP, 28 State Street, Boston, MA 02109 (US).	
		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).	
		<b>Published</b> <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM			
(57) Abstract			
Novel polynucleotides and the proteins encoded thereby are disclosed.			

**FOR THE PURPOSES OF INFORMATION ONLY**

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						



## 5           SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

This application is a continuation-in-part of the following applications:

- 10           (1)     provisional application Ser. No. 60/084,564, filed May 7, 1998;  
            (2)     provisional application Ser. No. 60/087,645, filed June 2, 1998;  
            (3)     provisional application Ser. No. 60/093,712, filed July 22, 1998;  
            (4)     provisional application Ser. No. 60/094,935, filed July 31, 1998;  
            (5)     provisional application Ser. No. 60/095,880, filed August 10, 1998;  
            (6)     provisional application Ser. No. 60/096,068, filed August 11, 1998;  
15   all of which are incorporated by reference herein.

FIELD OF THE INVENTION

20           The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

BACKGROUND OF THE INVENTION

25           Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression  
30   cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity by  
35   virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

### SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5           (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366;
- (c)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bn365\_53 deposited under accession  
10           number ATCC 98752;
- (d)     a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bn365\_53 deposited under accession number ATCC 98752;
- (e)     a polynucleotide comprising the nucleotide sequence of a mature  
15           protein coding sequence of clone bn365\_53 deposited under accession number ATCC 98752;
- (f)     a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bn365\_53 deposited under accession number ATCC 98752;
- (g)     a polynucleotide encoding a protein comprising the amino acid  
20           sequence of SEQ ID NO:2;
- (h)     a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;
- (i)     a polynucleotide which is an allelic variant of a polynucleotide of  
25           (a)-(f) above;
- (j)     a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k)     a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30           (l)     a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:1.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366; the nucleotide sequence of the full-length

protein coding sequence of clone bn365\_53 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone bn365\_53 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bn365\_53 deposited under accession number ATCC 98752. In further preferred  
5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding  
10 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

15 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize  
in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
20 consisting of:

(aa) SEQ ID NO:1, but excluding the poly(A) tail at the  
3' end of SEQ ID NO:1; and

(ab) the nucleotide sequence of the cDNA insert of clone  
bn365\_53 deposited under accession number ATCC 98752;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the  
probe(s);

and

30 (b) a process comprising the steps of:  
(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

(bb) the nucleotide sequence of the cDNA insert of clone bn365\_53 deposited under accession number ATCC 98752;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the  
15 cDNA sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:2;

25 (b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and

(c) the amino acid sequence encoded by the cDNA insert of clone bn365\_53 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2. In further preferred  
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5           (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915;
- (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915;
- 10          (d)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bo342\_2 deposited under accession number ATCC 98752;
- (e)     a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;
- 15          (f)     a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bo342\_2 deposited under accession number ATCC 98752;
- (g)     a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;
- 20          (h)     a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;
- (i)     a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;
- 25          (j)     a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k)     a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30          (l)     a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m)     a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:3.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915; the nucleotide sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915; the nucleotide sequence of the full-length protein coding sequence of clone bo342\_2 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone bo342\_2 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 280 to amino acid 289 of SEQ ID NO:4.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:3.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and
    - (ab) the nucleotide sequence of the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(bb) the nucleotide sequence of the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:3 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915.

30 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:4;

(b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and

(c) the amino acid sequence encoded by the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4. In further preferred  
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from  
10 amino acid 280 to amino acid 289 of SEQ ID NO:4.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dn721\_8 deposited under accession number ATCC 98752;
- 20 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dn721\_8 deposited under accession number ATCC 98752;
- 25 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;
- 30 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;



(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:5.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689; the nucleotide sequence of the full-length  
10 protein coding sequence of clone dn721\_8 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone dn721\_8 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752. In further preferred  
15 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a polynucleotide encoding  
20 biological activity, the fragment comprising the amino acid sequence from amino acid 318 to amino acid 327 of SEQ ID NO:6.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:5.

Further embodiments of the invention provide isolated polynucleotides produced  
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(ab) the nucleotide sequence of the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(bb) the nucleotide sequence of the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5, and extending  
20 contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:5 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689, and extending  
25 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689.

30 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:6;

(b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and

(c) the amino acid sequence encoded by the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:6. In further preferred  
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from  
10 amino acid 318 to amino acid 327 of SEQ ID NO:6.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dn834\_1 deposited under accession  
20 number ATCC 98752;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752;
- (f) a polynucleotide comprising the nucleotide sequence of a mature  
25 protein coding sequence of clone dn834\_1 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752;
- (h) a polynucleotide encoding a protein comprising the amino acid  
30 sequence of SEQ ID NO:8;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:7.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484; the nucleotide sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892; the nucleotide sequence of the full-length protein coding sequence of clone dn834\_1 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone dn834\_1 deposited  
15 under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological  
20 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 72 to amino acid 81 of SEQ ID NO:8.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

- (ab) the nucleotide sequence of the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 dn834\_1 deposited under accession number ATCC 98752;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated
- 25 according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 20 to
- 30 nucleotide 484. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide

18 to nucleotide 892, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 72 to amino acid 81 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pd278\_5 deposited under accession number ATCC 98752;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pd278\_5 deposited under accession number ATCC 98752;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

15 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:9.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420; the nucleotide sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420; the nucleotide sequence of the full-length  
20 protein coding sequence of clone pd278\_5 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pd278\_5 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752. In further preferred  
25 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having  
30 biological activity, the fragment comprising the amino acid sequence from amino acid 98 to amino acid 107 of SEQ ID NO:10.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:9.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(ab) the nucleotide sequence of the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(bb) the nucleotide sequence of the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:9 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420, and extending



contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
- (b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:10. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 98 to amino acid 107 of SEQ ID NO:10.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pe80\_1 deposited under accession number ATCC 98752;

- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pe80\_1 deposited under accession number ATCC 98752;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:11.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295; the nucleotide sequence of the full-length protein coding sequence of clone pe80\_1 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pe80\_1 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having

biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:12.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(ab) the nucleotide sequence of the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and

(bb) the nucleotide sequence of the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

25 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:11 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
- (b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:12.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm113\_1 deposited under accession number ATCC 98752;

5 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm113\_1 deposited under accession number ATCC 98752;

10 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

20 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:13.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428; the nucleotide sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428; the nucleotide sequence of the full-length protein coding sequence of clone pm113\_1 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pm113\_1 deposited  
30 under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological

activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 35  
5 to amino acid 44 of SEQ ID NO:14.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:13.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:13, but excluding the poly(A) tail at the  
15 3' end of SEQ ID NO:13; and
    - (ab) the nucleotide sequence of the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that  
25 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:13, but excluding the poly(A) tail at the  
3' end of SEQ ID NO:13; and
    - (bb) the nucleotide sequence of the cDNA insert of clone  
30 pm113\_1 deposited under accession number ATCC 98752;
  - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:13 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:14. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:14.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496;
- 5 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm749\_8 deposited under accession number ATCC 98752;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm749\_8 deposited under accession number ATCC 98752;
- 10 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm749\_8 deposited under accession number ATCC 98752;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm749\_8 deposited under accession number ATCC 98752;
- 15 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:15.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496; the nucleotide sequence of the full-length protein coding sequence of clone pm749\_8 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pm749\_8 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert

30



of clone pm749\_8 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 226 to amino acid 235 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
    - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (aa) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and
      - (ab) the nucleotide sequence of the cDNA insert of clone pm749\_8 deposited under accession number ATCC 98752;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (ba) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and
      - (bb) the nucleotide sequence of the cDNA insert of clone pm749\_8 deposited under accession number ATCC 98752;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).
- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:15 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15. Also preferably the
- 10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide
- 15 108 to nucleotide 1496.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
  - 20 (b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pm749\_8 deposited under accession number ATCC 98752;
- the protein being substantially free from other mammalian proteins. Preferably such
- 25 protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ
- 30 ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 226 to amino acid 235 of SEQ ID NO:16.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pt31\_4 deposited under accession number ATCC 98752;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pt31\_4 deposited under accession number ATCC 98752;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least
- 30 25% of the length of SEQ ID NO:17.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023; the nucleotide sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023; the nucleotide sequence of the full-length protein coding sequence of clone pt31\_4 deposited under accession number ATCC 98752; or the

nucleotide sequence of a mature protein coding sequence of clone pt31\_4 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 325 to amino acid 334 of SEQ ID NO:18.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:17.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

- (ab) the nucleotide sequence of the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

- (bb) the nucleotide sequence of the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:17 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 203, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 203, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 203. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 203, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 203, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 203.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 25 (a) the amino acid sequence of SEQ ID NO:18;
- (b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;
- 30

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:18. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 325 to amino acid 334 of SEQ ID NO:18.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pv296\_5 deposited under accession number ATCC 98752;
- 15 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pv296\_5 deposited under accession number ATCC 98752;
- 20 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- 25 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 30 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:19.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299; the nucleotide sequence of the full-length protein coding sequence of clone pv296\_5 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pv296\_5 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID NO:20.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:19.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
    - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (aa) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and
      - (ab) the nucleotide sequence of the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(bb) the nucleotide sequence of the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:19 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

25 (a) the amino acid sequence of SEQ ID NO:20;

(b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and

(c) the amino acid sequence encoded by the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752;

30 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:20. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably



comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID NO:20.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
10 NO:21 from nucleotide 8 to nucleotide 2008;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone er311\_20 deposited under accession number ATCC 98781;
- (d) a polynucleotide encoding the full-length protein encoded by the  
15 cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone er311\_20 deposited under accession number ATCC 98781;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA  
20 insert of clone er311\_20 deposited under accession number ATCC 98781;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment  
25 comprising eight contiguous amino acids of SEQ ID NO:22;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any  
30 one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:21.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008; the nucleotide sequence of the full-length protein coding sequence of clone er311\_20 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone er311\_20 deposited under accession number ATCC 98781. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 328 to amino acid 337 of SEQ ID NO:22.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:21.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
    - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (aa) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and
      - (ab) the nucleotide sequence of the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

(bb) the nucleotide sequence of the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:21 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:22;

(b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:22. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 328 to amino acid 337 of SEQ ID NO:22.

5           In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID  
10     NO:23 from nucleotide 484 to nucleotide 2043;
- (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043;
- (d)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fh149\_12 deposited under accession  
15     number ATCC 98781;
- (e)     a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;
- (f)     a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fh149\_12 deposited under accession number  
20     ATCC 98781;
- (g)     a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;
- (h)     a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:24;
- (i)     a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;
- (j)     a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k)     a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l)     a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:23.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043; the nucleotide sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043; the nucleotide sequence of the full-length protein coding sequence of clone fh149\_12 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone fh149\_12 deposited under accession number ATCC 98781. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 255 to amino acid 264 of SEQ ID NO:24.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:23.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and
    - (ab) the nucleotide sequence of the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(bb) the nucleotide sequence of the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:24;

- (b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and
- (c) the amino acid sequence encoded by the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:24. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:24, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 255 to amino acid 264 of SEQ ID NO:24.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:25 from nucleotide 143 to nucleotide 1099;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pc201\_6 deposited under accession number ATCC 98781;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pc201\_6 deposited under accession number ATCC 98781;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
- 30 insert of clone pc201\_6 deposited under accession number ATCC 98781;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:26;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:25.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099; the nucleotide sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099; the nucleotide sequence of the full-length protein coding sequence of clone pc201\_6 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone pc201\_6 deposited under accession number ATCC 98781. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 170 to amino acid 179 of SEQ ID NO:26.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:25.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:



(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

(ab) the nucleotide sequence of the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

(bb) the nucleotide sequence of the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:25 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide

47 to nucleotide 1099. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:26;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:26. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:26, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 170 to amino acid 179 of SEQ ID NO:26.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pl87\_1 deposited under accession number ATCC 98781;
- 30 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pl87\_1 deposited under accession number ATCC 98781;

- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pl87\_1 deposited under accession number ATCC 98781;
- 5 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pl87\_1 deposited under accession number ATCC 98781;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- 10 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 15 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:27.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259; the nucleotide sequence of the full-length protein coding sequence of clone pl87\_1 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone pl87\_1 deposited under accession number ATCC 98781. In other preferred embodiments, the
- 25 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pl87\_1 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most
- 30 preferably thirty) contiguous amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:28.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:27.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and
- (ab) the nucleotide sequence of the cDNA insert of clone pl87\_1 deposited under accession number ATCC 98781;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 pl87\_1 deposited under accession number ATCC 98781;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:27 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259, to a nucleotide  
5 sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:28;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone  
pl87\_1 deposited under accession number ATCC 98781;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
20 of SEQ ID NO:28, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:28.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284;
- (c) a polynucleotide comprising the nucleotide sequence of the full-  
30 length protein coding sequence of clone pm514\_4 deposited under accession number ATCC 98781;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm514\_4 deposited under accession number ATCC 98781;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:29.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284; the nucleotide sequence of the full-length protein coding sequence of clone pm514\_4 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone pm514\_4 deposited under accession number ATCC 98781. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 365 to amino acid 374 of SEQ ID NO:30.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:29.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

(ab) the nucleotide sequence of the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

25 (bb) the nucleotide sequence of the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:30;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:30. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:30, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 365 to amino acid 374 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 30 NO:31 from nucleotide 135 to nucleotide 1997;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone co155\_12 deposited under accession number ATCC 98808;



- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone co155\_12 deposited under accession number ATCC 98808;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:32;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:31.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997; the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997; the nucleotide sequence of the full-length protein coding sequence of clone co155\_12 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone co155\_12 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having

biological activity, the fragment comprising the amino acid sequence from amino acid 322 to amino acid 331 of SEQ ID NO:32.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:31.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10

(aa) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(ab) the nucleotide sequence of the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;

15

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25

(ba) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(bb) the nucleotide sequence of the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:31 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:32;
- (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
- (c) the amino acid sequence encoded by the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:32. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 322 to amino acid 331 of SEQ ID NO:32.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fn189\_13 deposited under accession number ATCC 98808;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fn189\_13 deposited under accession number ATCC 98808;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:34;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:33.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343; the nucleotide sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343; the nucleotide sequence of the full-length protein coding sequence of clone fn189\_13 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone fn189\_13 deposited under accession number ATCC 98808. In other preferred embodiments, the

30

polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:34.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:33.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(ab) the nucleotide sequence of the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(bb) the nucleotide sequence of the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:33 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33. Also preferably the
- 10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide
- 15 21 to nucleotide 1343. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343, to a nucleotide sequence corresponding to the 3' end of
- 20 said sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:34;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and
- (c) the amino acid sequence encoded by the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;

- the protein being substantially free from other mammalian proteins. Preferably such
- 30 protein comprises the amino acid sequence of SEQ ID NO:34. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:34.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5           (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide 557;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35 from nucleotide 235 to nucleotide 899;
- 10          (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone lv2\_47 deposited under accession number ATCC 98808;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone lv2\_47 deposited under accession number ATCC 98808;
- 15          (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone lv2\_47 deposited under accession number ATCC 98808;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone lv2\_47 deposited under accession number ATCC 98808;
- 20          (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;
- 25          (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30          (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:35.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide 557; the nucleotide sequence of SEQ ID NO:35 from nucleotide 235 to nucleotide 899; the nucleotide sequence of the full-length protein coding sequence of clone lv2\_47 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone lv2\_47 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone lv2\_47 deposited under accession number ATCC 98808. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36 from amino acid 58 to amino acid 164. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 77 to amino acid 86 of SEQ ID NO:36.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:35.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

- (ab) the nucleotide sequence of the cDNA insert of clone lv2\_47 deposited under accession number ATCC 98808;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and



- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and
- (bb) the nucleotide sequence of the cDNA insert of clone lv2\_47 deposited under accession number ATCC 98808;
- 10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35, and

15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:35 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide

20 557, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide 557, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide 557. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

25 NO:35 from nucleotide 235 to nucleotide 899, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 235 to nucleotide 899, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 235 to nucleotide 899.

In other embodiments, the present invention provides a composition comprising

30 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:36;
- (b) the amino acid sequence of SEQ ID NO:36 from amino acid 58 to amino acid 164;

- (c) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and
- (d) the amino acid sequence encoded by the cDNA insert of clone lv2\_47 deposited under accession number ATCC 98808;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:36 or the amino acid sequence of SEQ ID NO:36 from amino acid 58 to amino acid 164. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably
- 10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 77 to amino acid 86 of SEQ ID NO:36.

In one embodiment, the present invention provides a composition comprising an

15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499;
- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ml243\_1 deposited under accession number ATCC 98808;
- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ml243\_1 deposited under accession number ATCC 98808;
- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:38;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:37.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499; the nucleotide sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499; the nucleotide sequence of the full-length protein coding sequence of clone ml243\_1 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone ml243\_1 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:38.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:37.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(ab) the nucleotide sequence of the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(bb) the nucleotide sequence of the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:37 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide

104 to nucleotide 499. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from  
5 nucleotide 215 to nucleotide 499, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:38;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:38. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
20 of SEQ ID NO:38, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:38.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm96\_9 deposited under accession  
30 number ATCC 98808;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;

- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm96\_9 deposited under accession number ATCC 98808;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:39.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861; the nucleotide sequence of the full-length protein coding sequence of clone pm96\_9 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone pm96\_9 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 110 to amino acid 119 of SEQ ID NO:40.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:39.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

(ab) the nucleotide sequence of the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

25 (bb) the nucleotide sequence of the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861, to a nucleotide  
5 sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:40;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:40. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
20 of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 110 to amino acid 119 of SEQ ID NO:40.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
30 NO:41 from nucleotide 427 to nucleotide 762;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pu261\_1 deposited under accession number ATCC 98808;



- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pu261\_1 deposited under accession number ATCC 98808;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:41.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762; the nucleotide sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762; the nucleotide sequence of the full-length protein coding sequence of clone pu261\_1 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone pu261\_1 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having

biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:42.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:41.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10

(aa) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(ab) the nucleotide sequence of the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;

15

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25

(ba) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(bb) the nucleotide sequence of the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:42;
- (b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pw214\_15 deposited under accession number ATCC 98808;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pw214\_15 deposited under accession number ATCC 98808;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:44;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:43.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824; the nucleotide sequence of the full-length protein coding sequence of clone pw214\_15 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone pw214\_15 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID NO:44.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:43.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(ab) the nucleotide sequence of the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and

(bb) the nucleotide sequence of the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:44;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID NO:44.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qb56\_19 deposited under accession number ATCC 98808;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qb56\_19 deposited under accession number ATCC 98808;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:46;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:45.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383; the nucleotide sequence of the full-length protein coding sequence of clone qb56\_19 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone qb56\_19 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:46, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:46.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:45.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

15 (ab) the nucleotide sequence of the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

20 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and

(bb) the nucleotide sequence of the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).



Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:45 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:45, but  
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:45. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383, to a nucleotide  
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:46;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:46. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
25 of SEQ ID NO:46, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:46.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qc646\_1 deposited under accession number ATCC 98808;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qc646\_1 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:47.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273; the nucleotide sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273; the nucleotide sequence of the full-length protein coding sequence of clone qc646\_1 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone qc646\_1 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808. In further preferred

embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a polynucleotide encoding  
5 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 179 to amino acid 188 of SEQ ID NO:48.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:47.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
15 consisting of:

(aa) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

(ab) the nucleotide sequence of the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

(bb) the nucleotide sequence of the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide  
10 1273, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
15 NO:47 from nucleotide 242 to nucleotide 1273, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
- (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
- (c) the amino acid sequence encoded by the cDNA insert of clone  
25 qc646\_1 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48. In further preferred embodiments, the present invention provides a protein comprising a fragment of the  
30 amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 179 to amino acid 188 of SEQ ID NO:48.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qf116\_2 deposited under accession number ATCC 98808;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qf116\_2 deposited under accession number ATCC 98808;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:50;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least
- 30 25% of the length of SEQ ID NO:49.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097; the nucleotide sequence of the full-length protein coding sequence of clone qf116\_2 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone qf116\_2

deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 147 to amino acid 156 of SEQ ID NO:50.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:49.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
    - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (aa) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and
      - (ab) the nucleotide sequence of the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (ba) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

- (bb) the nucleotide sequence of the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ  
10 ID NO:49 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
15 of said sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
20 consisting of:

- (a) the amino acid sequence of SEQ ID NO:50;
- (b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
- (c) the amino acid sequence encoded by the cDNA insert of clone  
25 qf116\_2 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:50. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably  
30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 147 to amino acid 156 of SEQ ID NO:50.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qf662\_3 deposited under accession number ATCC 98808;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qf662\_3 deposited under accession number ATCC 98808;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:52;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:51.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741; the nucleotide sequence of SEQ ID NO:51



from nucleotide 595 to nucleotide 741; the nucleotide sequence of the full-length protein coding sequence of clone qf662\_3 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone qf662\_3 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 92 to amino acid 101 of SEQ ID NO:52.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:51.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and
    - (ab) the nucleotide sequence of the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51; and

(bb) the nucleotide sequence of the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:51 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
15 corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741. Also preferably the polynucleotide isolated according to the above  
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:52;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and

(c) the amino acid sequence encoded by the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:52. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 92 to amino acid 101 of SEQ ID NO:52.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone am748\_5 deposited under accession number ATCC 98817;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone am748\_5 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:53.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196; the nucleotide sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196; the nucleotide sequence of the full-length protein coding sequence of clone am748\_5 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone am748\_5 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 40 to amino acid 49 of SEQ ID NO:54.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(ab) the nucleotide sequence of the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

10 (bb) the nucleotide sequence of the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196, to a nucleotide  
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from  
30 nucleotide 1002 to nucleotide 1196, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:54;
- (b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and
- (c) the amino acid sequence encoded by the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:54. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably
- 10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 40 to amino acid 49 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an

15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310;
- 20 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cj507\_1 deposited under accession number ATCC 98817;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817;
- 25 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cj507\_1 deposited under accession number ATCC 98817;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817;
- 30 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:55.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310; the nucleotide sequence of the full-length protein coding sequence of clone cj507\_1 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cj507\_1 deposited under accession number ATCC 98817. In other preferred embodiments, the  
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most  
20 preferably thirty) contiguous amino acids of SEQ ID NO:56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 205 to amino acid 214 of SEQ ID NO:56.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
25 ID NO:55.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

- (ab) the nucleotide sequence of the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 cj507\_1 deposited under accession number ATCC 98817;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide
- 30 51 to nucleotide 1310.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:56;



- (b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and
- (c) the amino acid sequence encoded by the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:56, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 205 to amino acid 214 of SEQ ID NO:56.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cn922\_5 deposited under accession
- 20 number ATCC 98817;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
- 25 protein coding sequence of clone cn922\_5 deposited under accession number ATCC 98817;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a protein comprising the amino acid
- 30 sequence of SEQ ID NO:58;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:57.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328; the nucleotide sequence of the full-length protein coding sequence of clone cn922\_5 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cn922\_5 deposited under accession number ATCC 98817. In other preferred embodiments, the  
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most  
20 preferably thirty) contiguous amino acids of SEQ ID NO:58, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 184 to amino acid 193 of SEQ ID NO:58.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
25 ID NO:57.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and

- (ab) the nucleotide sequence of the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 cn922\_5 deposited under accession number ATCC 98817;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:57 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide
- 30 195 to nucleotide 1328.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:58;

- (b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and
- (c) the amino acid sequence encoded by the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:58. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:58, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 184 to amino acid 193 of SEQ ID NO:58.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw691\_11 deposited under accession
- 20 number ATCC 98817;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw691\_11 deposited under accession number
- 25 ATCC 98817;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a protein comprising the amino acid
- 30 sequence of SEQ ID NO:60;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:59.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942; the nucleotide sequence of the full-length protein coding sequence of clone cw691\_11 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cw691\_11 deposited under accession number ATCC 98817. In other preferred embodiments, the  
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most  
20 preferably thirty) contiguous amino acids of SEQ ID NO:60, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 139 to amino acid 148 of SEQ ID NO:60.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
25 ID NO:59.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and

- (ab) the nucleotide sequence of the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 cw691\_11 deposited under accession number ATCC 98817;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:59 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide
- 30 76 to nucleotide 942.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:60;

- (b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and
- (c) the amino acid sequence encoded by the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:60. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:60, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 139 to amino acid 148 of SEQ ID NO:60.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:61 from nucleotide 119 to nucleotide 1252;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1000\_2 deposited under accession number ATCC 98817;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw1000\_2 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
- 30 insert of clone cw1000\_2 deposited under accession number ATCC 98817;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:62;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:61.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252; the nucleotide sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252; the nucleotide sequence of the full-length protein coding sequence of clone cw1000\_2 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cw1000\_2 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 202 to amino acid 211 of SEQ ID NO:62.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:61.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:



(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(ab) the nucleotide sequence of the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(bb) the nucleotide sequence of the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:61 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide

11 to nucleotide 1252. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from  
5 nucleotide 119 to nucleotide 1252, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:62;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:62. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
20 of SEQ ID NO:62, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 202 to amino acid 211 of SEQ ID NO:62.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
30 NO:63 from nucleotide 451 to nucleotide 1296;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1640\_1 deposited under accession number ATCC 98817;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw1640\_1 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:64;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:63.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296; the nucleotide sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296; the nucleotide sequence of the full-length protein coding sequence of clone cw1640\_1 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cw1640\_1 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:64, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having

biological activity, the fragment comprising the amino acid sequence from amino acid 203 to amino acid 212 of SEQ ID NO:64.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:63.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

(ab) the nucleotide sequence of the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

(bb) the nucleotide sequence of the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:63 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:64;
- (b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and
- (c) the amino acid sequence encoded by the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:64. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:64, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 203 to amino acid 212 of SEQ ID NO:64.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:66;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:65.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827; the nucleotide sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827; the nucleotide sequence of the full-length protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide

30

encodes the full-length or a mature protein encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 122 to amino acid 131 of SEQ ID NO:66.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:65.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65; and

(ab) the nucleotide sequence of the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65; and

(bb) the nucleotide sequence of the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:65 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65. Also preferably the
- 10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide
- 15 66 to nucleotide 827. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827, to a nucleotide sequence corresponding to the 3' end of
- 20 said sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:66;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
- (c) the amino acid sequence encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;

- the protein being substantially free from other mammalian proteins. Preferably such
- 30 protein comprises the amino acid sequence of SEQ ID NO:66. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a protein comprising a fragment of the amino acid sequence of SEQ



ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 122 to amino acid 131 of SEQ ID NO:66.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
10 NO:67 from nucleotide 413 to nucleotide 529;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dd426\_1 deposited under accession number ATCC 98817;
- (e) a polynucleotide encoding the full-length protein encoded by the  
15 cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dd426\_1 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA  
20 insert of clone dd426\_1 deposited under accession number ATCC 98817;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:68;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment  
25 comprising eight contiguous amino acids of SEQ ID NO:68;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:67.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529; the nucleotide sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529; the nucleotide sequence of the full-length protein coding sequence of clone dd426\_1 deposited under accession number ATCC 98817; or the  
5 nucleotide sequence of a mature protein coding sequence of clone dd426\_1 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817. In further preferred  
10 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 58  
15 to amino acid 67 of SEQ ID NO:68.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:67.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:67, but excluding the poly(A) tail at the  
25 3' end of SEQ ID NO:67; and
    - (ab) the nucleotide sequence of the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and  
30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and

(bb) the nucleotide sequence of the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:67 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:68;

(b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and

(c) the amino acid sequence encoded by the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:68. In further preferred  
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence  
10 from amino acid 58 to amino acid 67 of SEQ ID NO:68.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone di393\_2 deposited under accession  
20 number ATCC 98817;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone di393\_2 deposited under accession number ATCC 98817;
- (f) a polynucleotide comprising the nucleotide sequence of a mature  
25 protein coding sequence of clone di393\_2 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone di393\_2 deposited under accession number ATCC 98817;
- (h) a polynucleotide encoding a protein comprising the amino acid  
30 sequence of SEQ ID NO:70;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:70;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:69.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543; the nucleotide sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543; the nucleotide sequence of the full-length protein coding sequence of clone di393\_2 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone di393\_2 deposited  
15 under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone di393\_2 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological  
20 activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 80 to amino acid 89 of SEQ ID NO:70.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:69.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and

- (ab) the nucleotide sequence of the cDNA insert of clone di393\_2 deposited under accession number ATCC 98817;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 di393\_2 deposited under accession number ATCC 98817;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:69 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide
- 30 31 to nucleotide 543. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from

nucleotide 88 to nucleotide 543, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:70;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone  
10 di393\_2 deposited under accession number ATCC 98817;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:70. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably  
15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 80 to amino acid 89 of SEQ ID NO:70.

In one embodiment, the present invention provides a composition comprising an  
20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dj167\_2 deposited under accession number ATCC 98818;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dj167\_2 deposited under accession number ATCC 98818;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:72;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:72;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:71.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356; the nucleotide sequence of the full-length protein coding sequence of clone dj167\_2 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone dj167\_2 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 195 to amino acid 204 of SEQ ID NO:72.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:71.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:



(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

(ab) the nucleotide sequence of the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

(bb) the nucleotide sequence of the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:71 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group

5 consisting of:

- (a) the amino acid sequence of SEQ ID NO:72;
- (b) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and
- (c) the amino acid sequence encoded by the cDNA insert of clone

10 dj167\_2 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:72. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably

15 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence from amino acid 195 to amino acid 204 of SEQ ID NO:72.

In one embodiment, the present invention provides a composition comprising an

20 isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490;

25 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dj167\_19 deposited under accession

30 number ATCC 207090;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090;

- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dj167\_19 deposited under accession number ATCC 207090;
- 5 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:74;
- 10 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 15 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:73.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490; the nucleotide sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490; the nucleotide sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343; the nucleotide sequence of the full-length protein coding sequence of clone dj167\_19 deposited under accession number ATCC 207090; or
- 25 the nucleotide sequence of a mature protein coding sequence of clone dj167\_19 deposited under accession number ATCC 207090. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a
- 30 protein comprising the amino acid sequence of SEQ ID NO:74 from amino acid 637 to amino acid 1036. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or

a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence from amino acid 513 to amino acid 522 of SEQ ID NO:74.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:73.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

(ab) the nucleotide sequence of the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

(bb) the nucleotide sequence of the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73, and

extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:73 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
5 corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490. Also preferably the polynucleotide isolated according to the  
10 above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490. Also  
15 preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343, to a nucleotide sequence corresponding to the 3' end of said  
20 sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:74;
- 25 (b) the amino acid sequence of SEQ ID NO:74 from amino acid 637 to amino acid 1036;
- (c) a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74; and
- (d) the amino acid sequence encoded by the cDNA insert of clone  
30 dj167\_19 deposited under accession number ATCC 207090;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:74 or the amino acid sequence of SEQ ID NO:74 from amino acid 637 to amino acid 1036. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence  
 5 from amino acid 513 to amino acid 522 of SEQ ID NO:74.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dw665\_4 deposited under accession  
 15 number ATCC 98818;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;
- (f) a polynucleotide comprising the nucleotide sequence of a mature  
 20 protein coding sequence of clone dw665\_4 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;
- (h) a polynucleotide encoding a protein comprising the amino acid  
 25 sequence of SEQ ID NO:76;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of  
 30 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:75.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441; the nucleotide sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441; the nucleotide sequence of the full-length protein coding sequence of clone dw665\_4 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone dw665\_4 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 223 to amino acid 232 of SEQ ID NO:76.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:75.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and
    - (ab) the nucleotide sequence of the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(bb) the nucleotide sequence of the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:75 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:76;



- (b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:76. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:76, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 223 to amino acid 232 of SEQ ID NO:76.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dx146\_12 deposited under accession
- 20 number ATCC 98818;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
- 25 protein coding sequence of clone dx146\_12 deposited under accession number ATCC 98818;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a protein comprising the amino acid
- 30 sequence of SEQ ID NO:78;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:77.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592; the nucleotide sequence of the full-length protein coding sequence of clone dx146\_12 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone dx146\_12 deposited under accession number ATCC 98818. In other preferred embodiments, the  
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most  
20 preferably thirty) contiguous amino acids of SEQ ID NO:78, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 247 to amino acid 256 of SEQ ID NO:78.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
25 ID NO:77.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

- (ab) the nucleotide sequence of the cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 dx146\_12 deposited under accession number ATCC 98818;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:77 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide
- 30 78 to nucleotide 1592.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;

- (b) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:78. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:78, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 247 to amino acid 256 of SEQ ID NO:78.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 20 NO:79 from nucleotide 337 to nucleotide 948;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dx219\_13 deposited under accession number ATCC 98818;
- (e) a polynucleotide encoding the full-length protein encoded by the
- 25 cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dx219\_13 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA
- 30 insert of clone dx219\_13 deposited under accession number ATCC 98818;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:80;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:79.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948; the nucleotide sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948; the nucleotide sequence of the full-length protein coding sequence of clone dx219\_13 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone dx219\_13 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 150 to amino acid 159 of SEQ ID NO:80.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:79.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

(ab) the nucleotide sequence of the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

(bb) the nucleotide sequence of the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide

19 to nucleotide 948. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:80;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:80. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:80, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 150 to amino acid 159 of SEQ ID NO:80.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286;
- 30 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fm3\_1 deposited under accession number ATCC 98818;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fm3\_1 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:82;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:81.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286; the nucleotide sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286; the nucleotide sequence of the full-length protein coding sequence of clone fm3\_1 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone fm3\_1 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:82, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the



fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:82.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:81.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(ab) the nucleotide sequence of the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(bb) the nucleotide sequence of the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:81 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:82;
- (b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and
- (c) the amino acid sequence encoded by the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:82. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:82, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:82.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone h225\_1 deposited under accession number ATCC 98818;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone h225\_1 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:84;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:83.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572; the nucleotide sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572; the nucleotide sequence of the full-length protein coding sequence of clone h225\_1 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone h225\_1 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide

30

encodes the full-length or a mature protein encoded by the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:84, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:84.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:83.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
    - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (aa) SEQ ID NO:83; and
      - (ab) the nucleotide sequence of the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (ba) SEQ ID NO:83; and
      - (bb) the nucleotide sequence of the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;
    - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:83 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:83. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572, and extending contiguously from a nucleotide sequence  
10 corresponding to the 5' end of said sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572, and  
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:84;
- (b) a fragment of the amino acid sequence of SEQ ID NO:84, the  
fragment comprising eight contiguous amino acids of SEQ ID NO:84; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:84. In further preferred  
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:84, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:84.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone kj320\_1 deposited under accession number ATCC 98818;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone kj320\_1 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:86;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:86;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:85.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210; the nucleotide sequence of SEQ ID NO:85

from nucleotide 505 to nucleotide 3210; the nucleotide sequence of the full-length protein coding sequence of clone kj320\_1 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone kj320\_1 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:86, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 465 to amino acid 474 of SEQ ID NO:86.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:85.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

(ab) the nucleotide sequence of the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

(bb) the nucleotide sequence of the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:85 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
15 corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210. Also preferably the polynucleotide isolated according to the above  
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:86;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and

(c) the amino acid sequence encoded by the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:86. In further preferred



embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:86, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 465 to amino acid 474 of SEQ ID NO:86.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ml236\_5 deposited under accession number ATCC 98818;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ml236\_5 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:88;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:87.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899; the nucleotide sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899; the nucleotide sequence of the full-length protein coding sequence of clone ml236\_5 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone ml236\_5 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:88.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:87.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and
- (ab) the nucleotide sequence of the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and

10 (bb) the nucleotide sequence of the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:87 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:87, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:87. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899, to a nucleotide  
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from  
30 nucleotide 522 to nucleotide 899, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:88;
- (b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and
- (c) the amino acid sequence encoded by the cDNA insert of clone  
5 ml236\_5 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably  
10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:88.

In one embodiment, the present invention provides a composition comprising an  
15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
20 NO:89 from nucleotide 399 to nucleotide 452;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pu282\_10 deposited under accession number ATCC 98818;
- (e) a polynucleotide encoding the full-length protein encoded by the  
25 cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pu282\_10 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA  
30 insert of clone pu282\_10 deposited under accession number ATCC 98818;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:90;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:89.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452; the nucleotide sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452; the nucleotide sequence of the full-length protein coding sequence of clone pu282\_10 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone pu282\_10 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 69 to amino acid 78 of SEQ ID NO:90.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:89.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

(ab) the nucleotide sequence of the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

(bb) the nucleotide sequence of the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:89 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide

6 to nucleotide 452. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:90;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:90. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:90, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 69 to amino acid 78 of SEQ ID NO:90.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179;
- 30 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone at94\_2 deposited under accession number ATCC 98822;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone at94\_2 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:92;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:91.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179; the nucleotide sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179; the nucleotide sequence of the full-length protein coding sequence of clone at94\_2 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone at94\_2 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the



fragment comprising the amino acid sequence from amino acid 191 to amino acid 200 of SEQ ID NO:92.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:91.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and

(ab) the nucleotide sequence of the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and

(bb) the nucleotide sequence of the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

ID NO:91 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:92;
- (b) a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92; and
- (c) the amino acid sequence encoded by the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:92. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 191 to amino acid 200 of SEQ ID NO:92.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bf169\_13 deposited under accession number ATCC 98822;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bf169\_13 deposited under accession number ATCC 98822;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:93.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077; the nucleotide sequence of the full-length protein coding sequence of clone bf169\_13 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone bf169\_13 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 332 to amino acid 341 of SEQ ID NO:94.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:93.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

(ab) the nucleotide sequence of the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

(bb) the nucleotide sequence of the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:93 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:94;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:94. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 332 to amino acid 341 of SEQ ID NO:94.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bl152\_12 deposited under accession number ATCC 98822;
- 5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bl152\_12 deposited under accession number ATCC 98822;
- 10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:96;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment  
15 comprising eight contiguous amino acids of SEQ ID NO:96;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:95.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735; the nucleotide sequence of the full-length protein coding sequence of clone bl152\_12 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone bl152\_12 deposited under accession number ATCC 98822. In other preferred embodiments, the  
30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:96, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 97 to amino acid 106 of SEQ ID NO:96.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:95.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and
    - 15 (ab) the nucleotide sequence of the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
  - 20 and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 25 (ba) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and
    - (bb) the nucleotide sequence of the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822;
  - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:95 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:95, but  
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:95. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735, to a nucleotide  
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:96;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone  
bl152\_12 deposited under accession number ATCC 98822;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:96. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
25 of SEQ ID NO:96, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 97 to amino acid 106 of SEQ ID NO:96.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816;



- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bz578\_1 deposited under accession number ATCC 98822;
- 5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bz578\_1 deposited under accession number ATCC 98822;
- 10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:98;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;
- 15 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:97.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816; the nucleotide sequence of the full-length protein coding sequence of clone bz578\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone bz578\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the
- 30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:98, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:98.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:97.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and
    - 15 (ab) the nucleotide sequence of the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- 20 and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 25 (ba) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and
    - (bb) the nucleotide sequence of the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822;
  - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:97, but  
5 excluding the poly(A) tail at the 3' end of SEQ ID NO:97. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816, to a nucleotide  
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:98;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:98. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
25 of SEQ ID NO:98, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:98.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99 from nucleotide 765 to nucleotide 992;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cb123\_1 deposited under accession number ATCC 98822;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cb123\_1 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:100;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:100;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:99.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992; the nucleotide sequence of SEQ ID NO:99 from nucleotide 765 to nucleotide 992; the nucleotide sequence of the full-length protein coding sequence of clone cb123\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone cb123\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822. In further preferred

embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:100, or a polynucleotide  
5 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:100.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:99.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize  
15 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:99, but excluding the poly(A) tail at the  
3' end of SEQ ID NO:99; and

(ab) the nucleotide sequence of the cDNA insert of clone  
cb123\_1 deposited under accession number ATCC 98822;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the  
probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that  
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from  
the group consisting of:

30 (ba) SEQ ID NO:99, but excluding the poly(A) tail at the  
3' end of SEQ ID NO:99; and

(bb) the nucleotide sequence of the cDNA insert of clone  
cb123\_1 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in  
conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:99 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99 from nucleotide  
10 992, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
15 NO:99 from nucleotide 765 to nucleotide 992, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:99 from nucleotide 765 to nucleotide 992, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide 765 to nucleotide 992.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:100;
- (b) a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100; and  
25 (c) the amino acid sequence encoded by the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:100. In further preferred embodiments, the present invention provides a protein comprising a fragment of the  
30 amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:100, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:100.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ch245\_1 deposited under accession number ATCC 98822;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ch245\_1 deposited under accession number ATCC 98822;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:101.
- 30

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480; the nucleotide sequence of the full-length protein coding sequence of clone ch245\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone ch245\_1

deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:102.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:101.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 20 (aa) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and
    - (ab) the nucleotide sequence of the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - 30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and



- (bb) the nucleotide sequence of the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:101 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:102;
- (b) a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:102. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:102.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cj378\_3 deposited under accession number ATCC 98822;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cj378\_3 deposited under accession number ATCC 98822;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:104;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least
- 30 25% of the length of SEQ ID NO:103.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541; the nucleotide sequence of the full-length protein coding sequence of clone cj378\_3 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone cj378\_3 deposited

under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822. In further preferred  
5 comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino  
10 acid 38 to amino acid 47 of SEQ ID NO:104.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:103.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 20 (aa) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and
    - (ab) the nucleotide sequence of the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- 30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and

- (bb) the nucleotide sequence of the cDNA insert of clone  
cj378\_3 deposited under accession number ATCC 98822;
- (ii) hybridizing said primer(s) to human genomic DNA in  
conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a  
nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103, and  
extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ  
10 ID NO:103 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:103, but  
excluding the poly(A) tail at the 3' end of SEQ ID NO:103. Also preferably the  
polynucleotide isolated according to the above process comprises a nucleotide sequence  
corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide  
541, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
15 of said sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541, to a nucleotide  
sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide  
281 to nucleotide 541.

In other embodiments, the present invention provides a composition comprising  
a protein, wherein said protein comprises an amino acid sequence selected from the group  
20 consisting of:

- (a) the amino acid sequence of SEQ ID NO:104;
- (b) a fragment of the amino acid sequence of SEQ ID NO:104, the  
fragment comprising eight contiguous amino acids of SEQ ID NO:104; and
- (c) the amino acid sequence encoded by the cDNA insert of clone  
25 cj378\_3 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such  
protein comprises the amino acid sequence of SEQ ID NO:104. In further preferred  
embodiments, the present invention provides a protein comprising a fragment of the  
amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably  
30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
of SEQ ID NO:104, or a protein comprising a fragment of the amino acid sequence of SEQ  
ID NO:104 having biological activity, the fragment comprising the amino acid sequence  
from amino acid 38 to amino acid 47 of SEQ ID NO:104.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1481\_1 deposited under accession number ATCC 98822;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw1481\_1 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:106;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:105.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202; the nucleotide sequence of SEQ ID

NO:105 from nucleotide 401 to nucleotide 2349; the nucleotide sequence of the full-length protein coding sequence of clone cw1481\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone cw1481\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 264 to amino acid 273 of SEQ ID NO:106.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:105.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and
    - (ab) the nucleotide sequence of the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

(bb) the nucleotide sequence of the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a  
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:105 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
15 corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202. Also preferably the polynucleotide isolated according to the above  
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:106;

(b) a fragment of the amino acid sequence of SEQ ID NO:106, the  
30 fragment comprising eight contiguous amino acids of SEQ ID NO:106; and

(c) the amino acid sequence encoded by the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:106. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 264 to amino acid 273 of SEQ ID NO:106.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dd119\_4 deposited under accession number ATCC 98822;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dd119\_4 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:108;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;



(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:107.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905; the nucleotide sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905; the nucleotide sequence of the full-length protein coding sequence of clone dd119\_4 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone dd119\_4 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:108, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 474 to amino acid 483 of SEQ ID NO:108.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:107.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and
    - (ab) the nucleotide sequence of the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and

(bb) the nucleotide sequence of the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:107 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:108;
- (b) a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:108. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably  
10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:108, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 474 to amino acid 483 of SEQ ID NO:108.

In one embodiment, the present invention provides a composition comprising an  
15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369;
- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone df202\_3 deposited under accession number ATCC 98822;
- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone df202\_3 deposited under accession number ATCC 98822;
- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:110;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:109.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369; the nucleotide sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369; the nucleotide sequence of the full-length protein coding sequence of clone df202\_3 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone df202\_3 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:110, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:110.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:109.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

(ab) the nucleotide sequence of the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

(bb) the nucleotide sequence of the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:109 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide

16 to nucleotide 369. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from  
5 nucleotide 103 to nucleotide 369, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:110;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:110. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
20 of SEQ ID NO:110, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:110.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
30 NO:111 from nucleotide 2255 to nucleotide 2539;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone km225\_1 deposited under accession number ATCC 98822;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone km225\_1 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:111.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539; the nucleotide sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539; the nucleotide sequence of the full-length protein coding sequence of clone km225\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone km225\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112

having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:112.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:111.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize  
10 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:111, but excluding the poly(A) tail at the  
3' end of SEQ ID NO:111; and

(ab) the nucleotide sequence of the cDNA insert of clone  
km225\_1 deposited under accession number ATCC 98822;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

(bb) the nucleotide sequence of the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ



ID NO:111 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:112;
- (b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and
- (c) the amino acid sequence encoded by the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:112. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:112.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 1734 to nucleotide 2030;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone mj301\_1 deposited under accession number ATCC 98822;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone mj301\_1 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:114;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:113.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:113 from nucleotide 1734 to nucleotide 2030; the nucleotide sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030; the nucleotide sequence of the full-length protein coding sequence of clone mj301\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone mj301\_1 deposited under accession number ATCC 98822. In other preferred

30

embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:114.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:113.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and

(ab) the nucleotide sequence of the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and

(bb) the nucleotide sequence of the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).
- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:113 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113. Also preferably the
- 10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113 from nucleotide 1734 to nucleotide 2030, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 1734 to nucleotide 2030, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:113
- 15 from nucleotide 1734 to nucleotide 2030. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030, to a nucleotide
- 20 sequence corresponding to the 3' end of said sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 25
- (a) the amino acid sequence of SEQ ID NO:114;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;
- 30 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:114. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids

of SEQ ID NO:114, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:114.

In one embodiment, the present invention provides a composition comprising an  
5 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350;
- 10 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ml10\_7 deposited under accession number ATCC 98822;
- 15 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ml10\_7 deposited under accession number ATCC 98822;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:116;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:115.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350; the nucleotide sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350; the nucleotide sequence of the full-length protein coding sequence of clone ml10\_7 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone ml10\_7 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:116, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 87 to amino acid 96 of SEQ ID NO:116.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:115.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and
    - (ab) the nucleotide sequence of the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and

(bb) the nucleotide sequence of the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:115 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:116;

- (b) a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:116. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:116, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 87 to amino acid 96 of SEQ ID NO:116.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone my340\_1 deposited under accession
- 20 number ATCC 98822;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822;
- (e) a polynucleotide comprising the nucleotide sequence of a mature
- 25 protein coding sequence of clone my340\_1 deposited under accession number ATCC 98822;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a protein comprising the amino acid
- 30 sequence of SEQ ID NO:118;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;



(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:117.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094; the nucleotide sequence of the full-length protein coding sequence of clone my340\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone my340\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the  
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most  
20 preferably thirty) contiguous amino acids of SEQ ID NO:118, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:118.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
25 ID NO:117.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117; and

- (ab) the nucleotide sequence of the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 15 my340\_1 deposited under accession number ATCC 98822;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:117 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117. Also preferably the
- 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:117 from nucleotide
- 30 837 to nucleotide 1094.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:118;

- (b) a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118; and
- (c) the amino acid sequence encoded by the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:118. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 10 of SEQ ID NO:118, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:118.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial,

15 yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

- 20 (a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and
- (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention.

25 Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically

30 effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

#### BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

### DETAILED DESCRIPTION

#### 5 ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full-length  
10 and mature forms) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available  
15 at the time of filing.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell  
20 in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

#### Clone "bn365\_53"

A polynucleotide of the present invention has been identified as clone "bn365\_53".  
25 bn365\_53 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bn365\_53 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein  
30 as "bn365\_53 protein").

The nucleotide sequence of bn365\_53 as presently determined is reported in SEQ ID NO:1, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bn365\_53 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bn365\_53 should be approximately 650 bp.

The nucleotide sequence disclosed herein for bn365\_53 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bn365\_53 demonstrated at least some similarity with sequences identified as AA242967 (zr65g11.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 668324 5') and N40141 (yw73c12.r1 Homo sapiens cDNA clone 257878 5'). The predicted amino acid sequence disclosed herein for bn365\_53 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bn365\_53 protein demonstrated at least some similarity to sequences identified as D63484 (KIAA0150 protein [Homo sapiens]) and to the GAGE-1 to GAGE-6 family of human proteins expressed in tumors (GenBank Accession Numbers U19142-U19147). The amino acid sequence of SEQ ID NO:2 contains two RGD (Arg-Gly-Asp) motifs (around residues 12 and 75): the sequence Arg-Gly-Asp, found in fibronectin, is crucial for its interaction with its cell surface receptor, an integrin. What has been called the 'RGD' tripeptide is also found in the sequences of a number of other proteins, where it has been shown to play a role in cell adhesion. These proteins are: some forms of collagens, fibrinogen, vitronectin, von Willebrand factor (VWF), snake disintegrins, and slime mold discoidins. Based upon sequence similarity, bn365\_53 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of bn365\_53 indicates that it may contain one or more repetitive elements.

#### Clone "bo342\_2"

A polynucleotide of the present invention has been identified as clone "bo342\_2". bo342\_2 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bo342\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bo342\_2 protein").

The nucleotide sequence of bo342\_2 as presently determined is reported in SEQ ID NO:3, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bo342\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:4. Amino

acids 372 to 384 of SEQ ID NO:4 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 385. Amino acids 1 to 13 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning in that case at amino acid 14. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the bo342\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bo342\_2 should be approximately 2600 bp.

The nucleotide sequence disclosed herein for bo342\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bo342\_2 demonstrated at least some similarity with sequences identified as AA306000 (EST177027 Jurkat T-cells VI Homo sapiens cDNA 5' end) and W94256 (ze12b02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358731 3' similar to contains Alu repetitive element). Based upon sequence similarity, bo342\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts six potential transmembrane domains within the bo342\_2 protein sequence, centered around amino acids 300, 320, 380, 410, 430, and 490 of SEQ ID NO:4, respectively. The nucleotide sequence of bo342\_2 indicates that it may contain Alu or other repetitive elements.

#### Clone "dn721\_8"

A polynucleotide of the present invention has been identified as clone "dn721\_8". dn721\_8 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dn721\_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dn721\_8 protein").

The nucleotide sequence of dn721\_8 as presently determined is reported in SEQ ID NO:5, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dn721\_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dn721\_8 should be approximately 2900 bp.

The nucleotide sequence disclosed herein for dn721\_8 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dn721\_8 demonstrated at least some similarity with sequences identified as H63637 (yr34b12.r1 Homo sapiens cDNA clone 207167 5'), N31598 (yy20b12.s1 Homo sapiens cDNA clone 271775 3'), and R61419 (yh15e05.r1 Homo sapiens cDNA clone 37671 5'). Based upon sequence similarity, dn721\_8 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two possible transmembrane domains within the dn721\_8 protein sequence, one centered around amino acid 269 and another around amino acid 457 of SEQ ID NO:6.

#### Clone "dn834\_1"

A polynucleotide of the present invention has been identified as clone "dn834\_1". dn834\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dn834\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dn834\_1 protein").

The nucleotide sequence of dn834\_1 as presently determined is reported in SEQ ID NO:7, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dn834\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:8.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dn834\_1 should be approximately 900 bp.

The nucleotide sequence disclosed herein for dn834\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dn834\_1 demonstrated at least some similarity with sequences identified as AA544005 (vj83h07.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone 935677 5'), AL022163 (Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 551E13; HTGS phase 1), L44560 (Homo sapiens thymus mRNA (randomly primed, normalized), single-pass sequence), and T72271 (Human B cell surface antigen cDNA). The predicted amino acid sequence disclosed herein for dn834\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the

BLASTX search protocol. The predicted dn834\_1 protein demonstrated at least some similarity to sequences identified as R47496 (Translated sequence of domains I and II of celD cDNA in clone pCNP4). Based upon sequence similarity, dn834\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the dn834\_1 protein sequence, centered around amino acids 59, 84, and 145 of SEQ ID NO:8, respectively.

dn834\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 18 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "pd278\_5"

A polynucleotide of the present invention has been identified as clone "pd278\_5". A cDNA clone was first isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate pd278\_5 from a human adult kidney cDNA library. pd278\_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pd278\_5 protein").

The nucleotide sequence of pd278\_5 as presently determined is reported in SEQ ID NO:9, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pd278\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10. Amino acids 61 to 73 of SEQ ID NO:10 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 74. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pd278\_5 protein.

There are two additional and mutually overlapping possible open reading frames close to the 5' end of SEQ ID NO:9 (bases 82 - 420 and bases 119 - 414). The translated open reading frame of bases 119 - 414 has a predicted leader/signal sequence from amino acid 49 to amino acid 61, with the predicted mature amino acid sequence beginning at



amino acid 62. Each of the additional possible open reading frames has a predicted transmembrane domain.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pd278\_5 should be approximately 2000 bp.

5 The nucleotide sequence disclosed herein for pd278\_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pd278\_5 demonstrated at least some similarity with sequences identified as AA292241 (zt50d11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 725781 5'), AA428245 zw51d10.s1 Soares total fetus Nb2HF8 9w Homo sapiens  
10 cDNA clone 773587 3'), AA599487 (ag23f05.s1 Jia bone marrow stroma Homo sapiens cDNA clone 1071201 3'), AA827135 (ob53b03.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE 1335053 3'), H54322 (yq90d03.s1 Homo sapiens cDNA clone 203045 3'), and T22170 (Human gene signature HUMGS03741). The predicted amino acid sequence disclosed herein for pd278\_5 was searched against the GenPept and GeneSeq amino acid  
15 sequence databases using the BLASTX search protocol. The predicted pd278\_5 protein demonstrated at least some similarity to sequences identified as R13144 (Deleted in Colorectal Carcinomas) and X13885 (extensin (AA 1-620) [Nicotiana tabacum]). Based upon sequence similarity, pd278\_5 proteins and each similar protein or peptide may share at least some activity.

20

#### Clone "pe80\_1"

A polynucleotide of the present invention has been identified as clone "pe80\_1". pe80\_1 was isolated from a human adult blood (chronic myelogenous leukemia K562) cDNA library using methods which are selective for cDNAs encoding secreted proteins  
25 (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pe80\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pe80\_1 protein").

The nucleotide sequence of pe80\_1 as presently determined is reported in SEQ ID  
30 NO:11, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pe80\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:12.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pe80\_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for pe80\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pe80\_1 demonstrated at least some similarity with sequences identified as AA291078 (zs47b04.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone  
5 IMAGE:700591 5'), AA429912 (zw66e06.s1 Soares testis NHT Homo sapiens cDNA clone 781186 3'), H82367 (yv79d06.r1 Homo sapiens cDNA clone 248939 5' similar to contains Alu repetitive element; contains OFR repetitive element), Q60627 (Human brain Expressed Sequence Tag EST02640), and R20261 (yg20a02.r1 Homo sapiens cDNA clone 32587 5').  
10 Based upon sequence similarity, pe80\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two possible transmembrane domains within the pe80\_1 protein sequence, one centered around amino acid 58 and another around amino acid 109 of SEQ ID NO:12. The nucleotide sequence of pe80\_1 indicates that it may contain an Alu repetitive element.

15 Clone "pm113\_1"

A polynucleotide of the present invention has been identified as clone "pm113\_1". pm113\_1 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis  
20 of computer analysis of the amino acid sequence of the encoded protein. pm113\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm113\_1 protein").

The nucleotide sequence of pm113\_1 as presently determined is reported in SEQ ID NO:13, and includes a poly(A) tail. What applicants presently believe to be the proper  
25 reading frame and the predicted amino acid sequence of the pm113\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14. Amino acids 41 to 53 of SEQ ID NO:14 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 54. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain  
30 should the predicted leader/signal sequence not be separated from the remainder of the pm113\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm113\_1 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for pm113\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pm113\_1 demonstrated at least some similarity with sequences identified as AA009482 (zi04c03.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429796 5'), AA350890 (EST58401 Infant brain Homo sapiens cDNA 3' end), AC003030 (Human DNA from chromosome 19-specific cosmid R29828, genomic sequence, complete sequence), H98961 (yx11b02.s1 Homo sapiens cDNA clone 261387 3'), R07796 (yf15e05.r1 Homo sapiens cDNA clone), T22151 (Human gene signature HUMGS03721), and W68491 (zd34h02.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 342579 5'). Based upon sequence similarity, pm113\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "pm749\_8"

A polynucleotide of the present invention has been identified as clone "pm749\_8". pm749\_8 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pm749\_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm749\_8 protein").

The nucleotide sequence of pm749\_8 as presently determined is reported in SEQ ID NO:15, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pm749\_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm749\_8 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for pm749\_8 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pm749\_8 demonstrated at least some similarity with sequences identified as AA314025 (EST185879 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end) and AA374458 (EST86612 HSC172 cells I Homo sapiens cDNA 5' end). The predicted amino acid sequence disclosed herein for pm749\_8 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol.

The predicted pm749\_8 protein demonstrated at least some similarity to sequences identified as D89169 (similar to *Saccharomyces cerevisiae* SCD6 protein, SWISS-PROT Accession Number P45978 [*Schizosaccharomyces pombe*]) and U30384 (Scd6p [*Saccharomyces cerevisiae*]). Based upon sequence similarity, pm749\_8 proteins and each  
5 similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pm749\_8 protein sequence centered around amino acid 138 of SEQ ID NO:16.

#### Clone "pt31\_4"

10 A polynucleotide of the present invention has been identified as clone "pt31\_4". pt31\_4 was isolated from a human adult blood (lymphoblastic leukemia MOLT-4) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pt31\_4  
15 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pt31\_4 protein").

The nucleotide sequence of pt31\_4 as presently determined is reported in SEQ ID NO:17, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pt31\_4 protein corresponding  
20 to the foregoing nucleotide sequence is reported in SEQ ID NO:18. Amino acids 19 to 31 of SEQ ID NO:18 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 32. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pt31\_4  
25 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pt31\_4 should be approximately 3200 bp.

The nucleotide sequence disclosed herein for pt31\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
30 FASTA search protocols. pt31\_4 demonstrated at least some similarity with sequences identified as AA348130 (EST54532 Fetal heart II *Homo sapiens* cDNA 5' end), AA350691 (EST58082 Infant brain *Homo sapiens* cDNA 5' end), AC001226 (Genomic sequence from Human 13, complete sequence), H22773 (ym54c06.r1 *Homo sapiens* cDNA clone 52351 5'), and R21869 (yh22b10.s1 *Homo sapiens* cDNA clone 130459 3'). The predicted amino

acid sequence disclosed herein for pt31\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pt31\_4 protein demonstrated at least some similarity to sequences identified as U53147 (C01B7.6 [Caenorhabditis elegans]). Based upon sequence similarity, pt31\_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five potential transmembrane domains within the pt31\_4 protein sequence, centered around amino acids 90, 110, 210, 410, and 590 of SEQ ID NO:18, respectively.

10        Clone "pv296\_5"

A polynucleotide of the present invention has been identified as clone "pv296\_5". pv296\_5 was isolated from a human adult brain (cerebellum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pv296\_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pv296\_5 protein").

The nucleotide sequence of pv296\_5 as presently determined is reported in SEQ ID NO:19, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pv296\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:20.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pv296\_5 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for pv296\_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pv296\_5 demonstrated at least some similarity with sequences identified as AA022471 (ze70c01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 364320 3'), AA335246 (EST39647 Epididymus Homo sapiens cDNA 5' end), and AA481308 (zv06a05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 752816 5'). Based upon sequence similarity, pv296\_5 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pv296\_5 protein sequence centered around amino acid 32 of SEQ ID NO:20.

Clone "er311\_20"

A polynucleotide of the present invention has been identified as clone "er311\_20". er311\_20 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. er311\_20 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "er311\_20 protein").

The nucleotide sequence of er311\_20 as presently determined is reported in SEQ  
10 ID NO:21, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the er311\_20 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:22. Amino acids 654 to 666 of SEQ ID NO:22 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 667. Due to the  
15 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the er311\_20 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone er311\_20 should be approximately 2800 bp.

20 The nucleotide sequence disclosed herein for er311\_20 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. er311\_20 demonstrated at least some similarity with sequences identified as AF035526 (Mus musculus kanadaplin mRNA, complete cds), R18277 (yg01c06.r1 Homo sapiens cDNA clone 31018 5' similar to SP:ZK632.2 CE00419  
25 COILED COIL PROTEIN), R47371 (Hf060-r Homo sapiens cDNA clone f060-r), and Z40133 (H. sapiens partial cDNA sequence; clone c-1sh08). The predicted amino acid sequence disclosed herein for er311\_20 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted er311\_20 protein demonstrated at least some similarity to sequences identified as  
30 AF035526 (kanadaplin [Mus musculus]) and Z22181 (ZK632.2 [Caenorhabditis elegans]). The mouse kanadaplin protein and the predicted er311\_20 protein both contain poly-glutamic acid stretches within their C-terminal portions. Based upon sequence similarity, er311\_20 proteins and each similar protein or peptide may share at least some activity.

The TopPredII computer program predicts two potential transmembrane domains within the er311\_20 protein sequence, one centered around amino acid 667 and another at the extreme C-terminus of SEQ ID NO:22.

er311\_20 protein was expressed in a COS cell expression system, and an expressed  
5 protein band of approximately 91 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "fh149\_12"

A polynucleotide of the present invention has been identified as clone "fh149\_12".  
10 fh149\_12 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fh149\_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein  
15 as "fh149\_12 protein").

The nucleotide sequence of fh149\_12 as presently determined is reported in SEQ ID NO:23, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the fh149\_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:24. Amino  
20 acids 133 to 145 of SEQ ID NO:24 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 146. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the fh149\_12 protein.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fh149\_12 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for fh149\_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fh149\_12 demonstrated at least some similarity with sequences  
30 identified as AA653557 (ag67b07.s1 Gessler Wilms tumor Homo sapiens cDNA clone 1127989 3'), AA191185 (zq45b09.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 632633 5'), H20588 (yn63d06.r1 Homo sapiens cDNA clone 173099 5'), R16294 (yf93b09.r1 Homo sapiens cDNA clone 30087 5'), T08702 (Rat OCT-1 gene),

T25120 (Human gene signature HUMGS07278), U38652 (Mus musculus transmembrane transporter (Lx1) mRNA, complete cds), U77086 (Human organic cation transporter 1 (hOCT1) mRNA, complete cds), and Z66539 (H.sapiens creatine transporter gene). The predicted amino acid sequence disclosed herein for fh149\_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted fh149\_12 protein demonstrated at least some similarity to sequences identified as D17546 (Collagen [Mus musculus]), R77676 (Rat OCT-1 protein), and U77086 (organic cation transporter 1 [Homo sapiens]). The fh149\_12 protein also shows some homology to organic cation transporters from rat (GenBank L27651) and pig (GenBank Y09400) cells. Based upon sequence similarity, fh149\_12 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts eleven potential transmembrane domains within the fh149\_12 protein sequence, centered around amino acids 40, 112, 139, 162, 200, 229, 349, 376, 405, 436, and 467 of SEQ ID NO:24, respectively.

#### Clone "pc201\_6"

A polynucleotide of the present invention has been identified as clone "pc201\_6". pc201\_6 was isolated from a human adult retina (retinoblastoma WERI-Rb1) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pc201\_6 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pc201\_6 protein").

The nucleotide sequence of pc201\_6 as presently determined is reported in SEQ ID NO:25, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pc201\_6 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:26. Amino acids 20 to 32 of SEQ ID NO:26 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 33. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pc201\_6 protein.



A partial cDNA clone related to pc201\_6, pc201\_SP, was also isolated from a human adult retina (retinoblastoma WERI-Rb1) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. The pc201\_SP clone appears to encode a splice variant of the pc201\_6 protein. The amino acid sequence of the predicted pc201\_SP splice variant protein comprises the amino acid sequence reported in SEQ ID NO:177.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pc201\_6 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for pc201\_6 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pc201\_6 demonstrated at least some similarity with sequences identified as AA256414 (zr80d11.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 682005 5' similar to WP EEED8.9 CE01893), AA342139 (EST47690 Fetal spleen Homo sapiens cDNA 3' end), AC004085 (Homo sapiens; HTGS phase 1, 72 unordered pieces), AF035950 (Homo sapiens putative DDB p127-associated protein mRNA, partial cds), and H10436 (ym08d09.s1 Homo sapiens cDNA clone 47394 3'). The predicted amino acid sequence disclosed herein for pc201\_6 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pc201\_6 protein demonstrated at least some similarity to sequences identified as AF035950 (putative DDB p127-associated protein [Homo sapiens]) and U23484 (EEED8.5 [Caenorhabditis elegans]). Based upon sequence similarity, pc201\_6 proteins and each similar protein or peptide may share at least some activity.

#### Clone "pl87\_1"

A polynucleotide of the present invention has been identified as clone "pl87\_1". pl87\_1 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pl87\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pl87\_1 protein").

The nucleotide sequence of pl87\_1 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pl87\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pl87\_1 should be approximately 700 bp.

The nucleotide sequence disclosed herein for pl87\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pl87\_1 demonstrated at least some similarity with sequences  
10 identified as AA371861 (EST83927 Parathyroid gland tumor I Homo sapiens cDNA 5' end) and AA861863 (ak39e11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1408364 3'). Based upon sequence similarity, pl87\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domains within the pl87\_1 protein sequence centered around amino acid  
15 50 of SEQ ID NO:28.

pl87\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 22 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### 20 Clone "pm514\_4"

A polynucleotide of the present invention has been identified as clone "pm514\_4". pm514\_4 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis  
25 of computer analysis of the amino acid sequence of the encoded protein. pm514\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm514\_4 protein").

The nucleotide sequence of pm514\_4 as presently determined is reported in SEQ ID NO:29, and includes a poly(A) tail. What applicants presently believe to be the proper  
30 reading frame and the predicted amino acid sequence of the pm514\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:30.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm514\_4 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for pm514\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pm514\_4 demonstrated at least some similarity with sequences identified as AA393855 (zv64g11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 758468 5' similar to WP ZK1248.14 CE02898), AA427943 (zw53d10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773779 3'), AA434561 (zw53d10.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773779 5'), W49736 (zc41a03.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324844 5'), and U95822 (Human putative transmembrane GTPase mRNA, partial cds). The predicted amino acid sequence disclosed herein for pm514\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pm514\_4 protein demonstrated at least some similarity to sequences identified as U95822 (putative transmembrane GTPase [Homo sapiens]). Based upon sequence similarity, pm514\_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pm514\_4 protein sequence, centered around amino acid 600 of SEQ ID NO:30.

#### Clone "co155\_12"

A polynucleotide of the present invention has been identified as clone "co155\_12". co155\_12 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. co155\_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "co155\_12 protein").

The nucleotide sequence of co155\_12 as presently determined is reported in SEQ ID NO:31, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the co155\_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:32. Amino acids 21 to 33 of SEQ ID NO:32 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 34. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain

should the predicted leader/signal sequence not be separated from the remainder of the co155\_12 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone co155\_12 should be approximately 2700 bp.

5 The nucleotide sequence disclosed herein for co155\_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. co155\_12 demonstrated at least some similarity with sequences identified as AA578373 (nl23d11.s1 NCI\_CGAP\_HSC1 Homo sapiens cDNA clone IMAGE:1041525, mRNA sequence), N43800 (yy42h09.r1 Homo sapiens cDNA clone  
10 273953 5'), and W40418 (zc82c10.r1 Pancreatic Islet Homo sapiens cDNA clone 328818 5', mRNA sequence). The predicted amino acid sequence disclosed herein for co155\_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted co155\_12 protein demonstrated at least some similarity to the sequences identified as L12721 (transmembrane domain encoded by  
15 1099-1167) and AF004849 (human serine/threonin protein kinase). Based upon sequence similarity, co155\_12 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential transmembrane domains within the co155\_12 protein sequence, centered around amino acids 90, 180, 470, 580, and 610 of SEQ ID NO:32, respectively.

20

#### Clone "fn189\_13"

A polynucleotide of the present invention has been identified as clone "fn189\_13". fn189\_13 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
25 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fn189\_13 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "fn189\_13 protein").

The nucleotide sequence of fn189\_13 as presently determined is reported in SEQ  
30 ID NO:33, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the fn189\_13 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:34. Amino acids 9 to 21 of SEQ ID NO:34 are a predicted leader/signal sequence, with the predicted

mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the fn189\_13 protein.

5       The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fn189\_13 should be approximately 3800 bp.

      The nucleotide sequence disclosed herein for fn189\_13 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fn189\_13 demonstrated at least some similarity with sequences  
10 identified as AA144270 (mr14d12.r1 Soares mouse 3NbMS Mus musculus cDNA clone 597431 5') and N27605 (yx44e10.r1 Homo sapiens cDNA clone 264618 5'). The predicted amino acid sequence disclosed herein for fn189\_13 was searched against the GenPept, GeneSeq, and SWISS\_PROT amino acid sequence databases using the BLASTX search protocol. The predicted fn189\_13 protein demonstrated at least some similarity to  
15 sequences identified as P32857 (PROTEIN PTM1 PRECURSOR [Saccharomyces cerevisiae]) and U64598 (weakly similar to S. cerevisiae PTM1 precursor (SP:P32857) [Caenorhabditis elegans]). Based upon sequence similarity, fn189\_13 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential transmembrane domains within the fn189\_13  
20 protein sequence, centered around amino acids 225, 260, 340, 360, and 420 of SEQ ID NO:34, respectively.

#### Clone "lv2\_47"

      A polynucleotide of the present invention has been identified as clone "lv2\_47".  
25 lv2\_47 was isolated from a human adult thyroid cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. lv2\_47 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as  
30 "lv2\_47 protein").

      The nucleotide sequence of lv2\_47 as presently determined is reported in SEQ ID NO:35, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the lv2\_47 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:36. The TopPredII

computer program predicts a potential transmembrane domain within the lv2\_47 protein sequence of SEQ ID NO:36, centered around amino acid 60.

Another potential lv2\_47 reading frame and predicted amino acid sequence is encoded by basepairs 365 to 880 of SEQ ID NO:35 and is reported in SEQ ID NO:178.

- 5 Amino acids 49 to 61 of SEQ ID NO:178 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 62. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:178. The TopPredII computer program predicts two additional potential
- 10 transmembrane domains within the SEQ ID NO:178 amino acid sequence.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone lv2\_47 should be approximately 1950 bp.

- The nucleotide sequence disclosed herein for lv2\_47 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and
- 15 FASTA search protocols. lv2\_47 demonstrated at least some similarity with sequences identified as AA007293 (zh97f07.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429253 5'), AA447347 (zw93g06.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784570 5' similar to WP:F43E2.7 CE07243), AA522451 (ng30h09.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:936353), AA526614 (ni52g12.s1
- 20 NCI\_CGAP\_Ov2 Homo sapiens cDNA clone 980518), F18178 (H.sapiens EST sequence (002-T4-28) from skeletal muscle, mRNA sequence), H46569 (yo20f10.s1 Homo sapiens cDNA clone 178507 3'), and T22574 (Human gene signature HUMGS04190). Based upon sequence similarity, lv2\_47 proteins and each similar protein or peptide may share at least some activity.

25

#### Clone "ml243\_1"

- A polynucleotide of the present invention has been identified as clone "ml243\_1". ml243\_1 was isolated from a human adult brain (caudate nucleus) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No.
- 30 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ml243\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ml243\_1 protein").

The nucleotide sequence of ml243\_1 as presently determined is reported in SEQ ID NO:37, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ml243\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:38. Amino acids 25 to 37 of SEQ ID NO:38 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 38. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ml243\_1 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ml243\_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for ml243\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ml243\_1 demonstrated at least some similarity with sequences identified as N66656 (yy71a06.s1 Homo sapiens cDNA clone 278962 3'), R17513 (yg02g12.r1 Homo sapiens cDNA clone 31064 5'), Z83837 (Human DNA sequence from Fosmid 113D11 on chromosome 22q11.2-qter contains ESTs, CpG island), and Z84468 (Human DNA sequence from clone 299D3; HTGS phase 1). Based upon sequence similarity, ml243\_1 proteins and each similar protein or peptide may share at least some activity.

20 ml243\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 16 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

#### 25 Clone "pm96\_9"

A polynucleotide of the present invention has been identified as clone "pm96\_9". pm96\_9 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pm96\_9 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm96\_9 protein").

The nucleotide sequence of pm96\_9 as presently determined is reported in SEQ ID NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pm96\_9 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:40.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm96\_9 should be approximately 3600 bp.

The nucleotide sequence disclosed herein for pm96\_9 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pm96\_9 demonstrated at least some similarity with sequences  
10 identified as AA444024 (zv44d12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 756503 5'), AA488901 (aa55h09.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:824897 3'), R16408 (yf40b02.r1 Homo sapiens cDNA clone 129291 5'), T19732 (Human gene signature HUMGS00806), U52112 (Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1  
15 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene), and Z82250 (Human DNA sequence from cosmid N86D4 on chromosome 22q12-qter contains STS). Based upon sequence similarity, pm96\_9 proteins and each similar protein  
20 or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain at the extreme C-terminus of the pm96\_9 protein sequence (SEQ ID NO:40).

#### Clone "pu261\_1"

25 A polynucleotide of the present invention has been identified as clone "pu261\_1". pu261\_1 was isolated from a human adult blood (promyelocytic leukemia HL-60) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein.  
30 pu261\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pu261\_1 protein").

The nucleotide sequence of pu261\_1 as presently determined is reported in SEQ ID NO:41, and includes a poly(A) tail. What applicants presently believe to be the proper



reading frame and the predicted amino acid sequence of the pu261\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42. Amino acids 116 to 128 of SEQ ID NO:42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 129. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pu261\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pu261\_1 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for pu261\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pu261\_1 demonstrated at least some similarity with sequences identified as H16093 (ym20g10.r1 Homo sapiens cDNA clone 48582 5'). Based upon sequence similarity, pu261\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the pu261\_1 protein sequence centered around amino acid 70 of SEQ ID NO:42.

#### Clone "pw214\_15"

A polynucleotide of the present invention has been identified as clone "pw214\_15". pw214\_15 was isolated from a human adult brain (cerebellum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pw214\_15 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pw214\_15 protein").

The nucleotide sequence of pw214\_15 as presently determined is reported in SEQ ID NO:43, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pw214\_15 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:44.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pw214\_15 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for pw214\_15 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. pw214\_15 demonstrated at least some similarity with sequences identified as AA173391 (zp03a07.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 595284 5'), AA253067 (zr52a10.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 667002 5'), AA523652 ni64d09.s1 NCI\_CGAP\_Pr12 Homo sapiens cDNA clone 981617), and H41832 (yo07b08.r1 Homo sapiens cDNA clone 177207 5'). Based upon sequence similarity, pw214\_15 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pw214\_15 protein sequence centered around amino acid 15 of SEQ ID NO:44.

10

#### Clone "qb56\_19"

A polynucleotide of the present invention has been identified as clone "qb56\_19". qb56\_19 was isolated from a human adult bladder (carcinoma 5637) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qb56\_19 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qb56\_19 protein").

The nucleotide sequence of qb56\_19 as presently determined is reported in SEQ ID NO:45, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qb56\_19 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:46. Amino acids 18 to 40 of SEQ ID NO:46 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 41. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qb56\_19 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qb56\_19 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for qb56\_19 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qb56\_19 demonstrated at least some similarity with sequences identified as AA632658 (np87c12.s1 NCI\_CGAP\_Thy1 Homo sapiens cDNA clone

IMAGE:1133302), N56430 (JJ8973F Homo sapiens cDNA clone JJ8973 5'), and W05470 (za87f11.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 299565 5'). Based upon sequence similarity, qb56\_19 proteins and each similar protein or peptide may share at least some activity.

- 5 qb56\_19 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 14 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "qc646\_1"

- 10 A polynucleotide of the present invention has been identified as clone "qc646\_1". qc646\_1 was isolated from a human adult neural tissue (neuroepithelioma HTB-10 line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded  
15 protein. qc646\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qc646\_1 protein").

- The nucleotide sequence of qc646\_1 as presently determined is reported in SEQ ID NO:47, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qc646\_1 protein  
20 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Amino acids 12 to 24 of SEQ ID NO:48 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 25. Amino acids 32 to 44 are also a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 45, or are a transmembrane domain. Due to the hydrophobic  
25 nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the qc646\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qc646\_1 should be approximately 1800 bp.

- The nucleotide sequence disclosed herein for qc646\_1 was searched against the  
30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qc646\_1 demonstrated at least some similarity with sequences identified as AA470035 (zt94a07.r1 Soares testis NHT Homo sapiens cDNA clone 729972 5'), and AA483957 (ne76e11.s1 NCI\_CGAP\_Ew1 Homo sapiens cDNA clone

IMAGE:910220). The predicted amino acid sequence disclosed herein for qc646\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted qc646\_1 protein demonstrated at least some similarity to sequences identified as D88666 (PS-PLA1 (serine phospholipid-specific phospholipase A) [Rattus norvegicus]), M93284 (lipase related protein 2 [Homo sapiens]), and R30739 (C-terminally truncated GPL(1-319)), as well as lipases from various other species. Rat PS-PLA1, serine phospholipid-specific phospholipase A, is a member of the lipase family and is secreted from activated platelets. Based upon sequence similarity, qc646\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the qc646\_1 protein sequence, one centered around amino acid 190 and another around amino acid 325 of SEQ ID NO:48. The nucleotide sequence of qc646\_1 indicates that it may contain Alu repetitive elements.

#### Clone "qf116\_2"

A polynucleotide of the present invention has been identified as clone "qf116\_2". qf116\_2 was isolated from a human adult bladder (carcinoma 5637) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qf116\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qf116\_2 protein").

The nucleotide sequence of qf116\_2 as presently determined is reported in SEQ ID NO:49, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qf116\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:50.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qf116\_2 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for qf116\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qf116\_2 demonstrated at least some similarity with sequences identified as D50810 (placental leucine aminopeptidase [Homo sapiens]), R94512 (GTVap (short version), insulin-cleaving aminopeptidase from GLUT-4 vesicles), and U32990

(vp165 [*Rattus norvegicus*]). Human placental leucine aminopeptidase/oxytocinase (P-LAP), a member of the type II membrane-spanning zinc metallopeptidase family, degrades several peptide hormones such as oxytocin and vasopresin, suggesting a role in maintaining homeostasis during pregnancy. The predicted P-LAP amino acid sequence contains the HEXXH consensus sequence of zinc metallopeptidases, indicating that the enzyme belongs to this family, which includes aminopeptidase N and aminopeptidase A. The deduced P-LAP amino acid sequence also contains a hydrophobic region near the N-terminus, suggesting that the enzyme is a type II integral membrane protein. Results suggest that the enzyme is synthesized as an integral membrane protein and is released into blood under some physiological conditions. (See Røgi *et al.*, 1996, *J. Biol. Chem.* 271(1): 56-61, which is incorporated by reference herein.) Based upon sequence similarity, qf116\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the qf116\_2 protein sequence, one centered around amino acid 25 and another around amino acid 290 of SEQ ID NO:50.

#### Clone "qf662\_3"

A polynucleotide of the present invention has been identified as clone "qf662\_3". qf662\_3 was isolated from a human adult bladder (carcinoma 5637) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qf662\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qf662\_3 protein").

The nucleotide sequence of qf662\_3 as presently determined is reported in SEQ ID NO:51, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qf662\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:52. Amino acids 133 to 145 of SEQ ID NO:52 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 146. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qf662\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qf662\_3 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for qf662\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qf662\_3 demonstrated no significant similarity with sequences in these databases. The nucleotide sequence of qf662\_3 indicates that it may contain repetitive elements.

Clone "am748\_5"

A polynucleotide of the present invention has been identified as clone "am748\_5". am748\_5 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. am748\_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "am748\_5 protein").

The nucleotide sequence of am748\_5 as presently determined is reported in SEQ ID NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the am748\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:54. Amino acids 14 to 26 of SEQ ID NO:54 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the am748\_5 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone am748\_5 should be approximately 1550 bp.

The nucleotide sequence disclosed herein for am748\_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. am748\_5 demonstrated at least some similarity with sequences identified as AA418860 (zv98g04.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 767862 5' similar to gb:X14008\_ma1 LYSOZYME C PRECURSOR (HUMAN); contains Alu repetitive element; contains element PTR5 repetitive element), AC003007 (Human

Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence), H73304 (yu27c10.r1 Homo sapiens cDNA clone 235026 5' similar to contains Alu repetitive element), N35175 (yx83d10.r1 Homo sapiens cDNA clone 268339 5' similar to gb X14008\_ma1 LYSOZYME C PRECURSOR (HUMAN); contains Alu repetitive element),  
5 N41479 (yy05a11.r1 Homo sapiens cDNA clone 270332 5' similar to gb:X14008\_ma1 LYSOZYME C PRECURSOR (HUMAN)), Q81139 (HPLA2-8 gene), T04964 (EST02852 Homo sapiens cDNA clone HFBCI77), and U18391 (Human Alu sequence clone A8). The predicted amino acid sequence disclosed herein for am748\_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol.  
10 The predicted am748\_5 protein demonstrated at least some similarity to sequences identified as X55777 (put. ORF [Homo sapiens]) and R13556 (Protein encoded downstream of hhc\_M oncoprotein). Based upon sequence similarity, am748\_5 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of am748\_5 indicates that it may contain one or more of the following repetitive  
15 elements: Alu, L1.

Clone "cj507\_1"

A polynucleotide of the present invention has been identified as clone "cj507\_1". cj507\_1 was isolated from a human fetal brain cDNA library using methods which are  
20 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cj507\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cj507\_1 protein").

25 The nucleotide sequence of cj507\_1 as presently determined is reported in SEQ ID NO:55, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cj507\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:56.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
30 cj507\_1 should be approximately 2100 bp.

The nucleotide sequence disclosed herein for cj507\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cj507\_1 demonstrated at least some similarity with sequences

identified as AA100356 (zn46a02.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 550442 5' similar to contains element PTR5 repetitive element), AA228100 (zr56g04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667446 3'), AA479997 (zv18b07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753973 5' similar to contains  
5 element PTR5 repetitive element, mRNA sequence), and X85324 (H.sapiens mRNA for non polymorphic CAG repeat (CAG12)). Based upon sequence similarity, cj507\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the cj507\_1 protein sequence centered around amino acid 265 of SEQ ID NO:56. The  
10 nucleotide sequence of cj507\_1 indicates that it may contain a GCA simple repeat region.

cj507\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 47 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

15        Clone "cn922\_5"

A polynucleotide of the present invention has been identified as clone "cn922\_5". cn922\_5 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
20 analysis of the amino acid sequence of the encoded protein. cn922\_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cn922\_5 protein").

The nucleotide sequence of cn922\_5 as presently determined is reported in SEQ ID NO:57, and includes a poly(A) tail. What applicants presently believe to be the proper  
25 reading frame and the predicted amino acid sequence of the cn922\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:58.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cn922\_5 should be approximately 2200 bp.

The nucleotide sequence disclosed herein for cn922\_5 was searched against the  
30 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cn922\_5 demonstrated at least some similarity with sequences identified as H34191 (EST110864 Rattus sp. cDNA 5' end), R18707 (yf98f02.r1 Homo sapiens cDNA clone 30546 5'), T26556 (Human gene signature HUMGS08801), and



Z83230 (*Caenorhabditis elegans* cosmid F56A8). The predicted amino acid sequence disclosed herein for cn922\_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cn922\_5 protein demonstrated at least some similarity to sequences identified as AB004535  
5 (HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION [Schizosaccharomyces pombe]) and Z83230 (F56A8.a and F56A8.1 [Caenorhabditis elegans]). Based upon sequence similarity, cn922\_5 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts six potential transmembrane domains within the cn922\_5 protein sequence, centered around  
10 amino acids 25, 100, 135, 190, 290, and 370 of SEQ ID NO:58, respectively. The nucleotide sequence of cn922\_5 indicates that it may contain one or more of the following repetitive elements: MER, L1.

Clone "cw691\_11"

15 A polynucleotide of the present invention has been identified as clone "cw691\_11". cw691\_11 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cw691\_11 is a full-length  
20 clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw691\_11 protein").

The nucleotide sequence of cw691\_11 as presently determined is reported in SEQ ID NO:59, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cw691\_11 protein  
25 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:60.

Another potential cw691\_11 reading frame and predicted amino acid sequence is encoded by basepairs 542 to 970 of SEQ ID NO:59 and is reported in SEQ ID NO:179. Amino acids 34 to 46 of SEQ ID NO:179 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 47. Due to the  
30 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:179.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw691\_11 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for cw691\_11 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw691\_11 demonstrated at least some similarity with sequences identified as AA363712 (EST74158 Pancreas I Homo sapiens cDNA 5' end similar to similar to *C. elegans* hypothetical protein R10E12.1), AA521201 (aa74c10.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone 826674 3'), AA527142 (ni07a10.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA clone IMAGE 967290, mRNA sequence), AA745501 (ny64d03.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1283045, mRNA sequence), N73108 (yv69a09.r1 Homo sapiens cDNA clone 247960 5'), T19938 (Human gene signature HUMGS01070), and W77963 (zd70d09.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 346001 5' similar to WP:R10E12.1 CE00310). The predicted amino acid sequence disclosed herein for cw691\_11 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw691\_11 protein demonstrated at least some similarity to sequences identified as P82971 (Bioadhesive precursor protein from cDNA 52), U73679 (YNK1-a [*Caenorhabditis elegans*]), and Z29561 (R10E12.1 [*Caenorhabditis elegans*]). Based upon sequence similarity, cw691\_11 proteins and each similar protein or peptide may share at least some activity.

#### Clone "cw1000\_2"

A polynucleotide of the present invention has been identified as clone "cw1000\_2". cw1000\_2 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cw1000\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw1000\_2 protein").

The nucleotide sequence of cw1000\_2 as presently determined is reported in SEQ ID NO:61, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cw1000\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:62. Amino

acids 24 to 36 of SEQ ID NO:62 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 37. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cw1000\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1000\_2 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for cw1000\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw1000\_2 demonstrated at least some similarity with sequences identified as AA446779 (zw89d11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784149 5', mRNA sequence), AA493561 (nh04f07.s1 NCI\_CGAP\_Thy1 Homo sapiens cDNA clone 943333 similar to WP:F15G9.4 CE01552 IG SUPERFAMILY REPEATS ;contains element MSR1 repetitive element), H35690 (EST111696 Rattus sp. cDNA similar to Opioid binding protein/cell adhesion-like molecule), R18502 (yf96a05.r1 Homo sapiens cDNA clone 30376 5'), T21582 (Human gene signature HUMGS02965), T39504 (ya06g11.r1 Homo sapiens cDNA clone 60740 5'), T46848 (yb94b01.r1 Homo sapiens cDNA clone 78793 5'), T51129 (yb94b01.s1 Homo sapiens cDNA clone 78793 3'), and W67535 (zd40g11.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 343172 3' similar to PIR S05539 S05539 glycophorin C - human ;contains element MSR1 repetitive element). The predicted amino acid sequence disclosed herein for cw1000\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw1000\_2 protein demonstrated at least some similarity to sequences identified as M24406 (poliovirus receptor [Homo sapiens]), R07130 (H2OB receptor), W04404 (Human CRTAM; Cytotoxic or Regulatory T-cell associated Mol.; CRTAM), X13890 (glycophorin C [Homo sapiens]), and X90569 (elastic titin [Homo sapiens]). Based upon sequence similarity, cw1000\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the cw1000\_2 protein sequence centered around amino acid 358 of SEQ ID NO:62. The nucleotide sequence of cw1000\_2 indicates that it may contain a GCC1 repeat element.

cw1000\_2 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 57 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

5        Clone "cw1640\_1"

A polynucleotide of the present invention has been identified as clone "cw1640\_1". cw1640\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
10 analysis of the amino acid sequence of the encoded protein. cw1640\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw1640\_1 protein").

The nucleotide sequence of cw1640\_1 as presently determined is reported in SEQ ID NO:63, and includes a poly(A) tail. What applicants presently believe to be the proper  
15 reading frame and the predicted amino acid sequence of the cw1640\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:64. Amino acids 123 to 135 of SEQ ID NO:64 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 136. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a  
20 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cw1640\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1640\_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for cw1640\_1 was searched against the  
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw1640\_1 demonstrated at least some similarity with sequences identified as AA075643 (zm88a12.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 544990 5' similar to SW:ACT\_EUPCR P20360 ACTIN), AA411334 (zv29e11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755084 5' similar to  
30 WP:C49H3.8 CE04234 ACTIN-LIKE PROTEIN ), AA913364 (ol37b07.s1 Soares NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1525621 3' similar to WP:C49H3.8 CE04234 ACTIN-LIKE PROTEIN, mRNA sequence), N25416 (yx40g10.r1 Homo sapiens cDNA clone 264258 5' similar to SP ACT2\_PLAFA P14883 ACTIN), R96887

(yq61g10.r1 Homo sapiens cDNA clone 200322 5'), W37097 (zb98h03.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320885 5'), W44778 (zb98h03.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320885 3'), W61038 (zc54g09.r1 Soares senescent fibroblasts NbHSF Homo), W76570 (zd66f12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 345647 5' similar to SW:ACT\_PROCL P45521 ACTIN), and W82519 (mf05b01.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone). The predicted amino acid sequence disclosed herein for cw1640\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw1640\_1 protein demonstrated at least some similarity to sequences identified as J00068 (alpha-actin [Homo sapiens]), J01163 (actin [Oxytricha fallax]), R22026 (A. chrysogenum actin), R50328 (Drug resistant structural protein), U42436 (Similar to actin-like protein [Caenorhabditis elegans]), and U90439 (actin isolog [Arabidopsis thaliana]). Based upon sequence similarity, cw1640\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "d24\_1"

A polynucleotide of the present invention has been identified as clone "d24\_1". A cDNA clone was first isolated from a human adult blood (peripheral blood mononuclear cells treated with concanavalin A and phorbol myristate acetate) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate d24\_1 from a human adult blood (peripheral blood mononuclear cells treated with phytohemagglutinin, phorbol myristate acetate, and mixed lymphocyte reaction) cDNA library. d24\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "d24\_1 protein").

The nucleotide sequence of d24\_1 as presently determined is reported in SEQ ID NO:65, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the d24\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:66. Amino acids 124 to 136 of SEQ ID NO:66 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 137. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should

the predicted leader/signal sequence not be separated from the remainder of the d24\_1 protein. The mRNA sequence encoding amino acids 172 to 175 of SEQ ID NO:66 may not be present in alternatively-spliced forms of d24\_1 mRNA molecules.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
5 d24\_1 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for d24\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. d24\_1 demonstrated at least some similarity with sequences identified as AA478740 (zv14g12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone  
10 753670 3'), AA479444 (zv14g12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753670 5', mRNA sequence), AA278581 (zs76f09.r1 Soares NbHTGBC Homo sapiens cDNA clone 703433 5' similar to WP T04A8.12 CE01067 YEAST 107.9KD PGK1-MAK32 INTERGENIC HYPOTHETICAL PROTEIN), H05202 (yl85h02.r1 Homo sapiens cDNA clone 45213 5' similar to SP T04A8.12m CE01067 YEAST 107.9KD  
15 PGK1-MAK32 INTERGENIC HYPOTHETICAL PROTEIN), R74287 (yi57e07.r1 Homo sapiens cDNA clone 143364 5'), U57715 (*Rattus norvegicus* FGF receptor activating protein FRAG1 (FRAG1) mRNA, complete CDs), and Z35663 (*C. elegans* protein of unknown function). The predicted amino acid sequence disclosed herein for d24\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the  
20 BLASTX search protocol. The predicted d24\_1 protein demonstrated at least some similarity to the sequence identified as U57715 (FGF receptor activating protein FRAG1 [*Rattus norvegicus*]). Lorenzi *et al.* (1996, *Proc. Natl. Acad. Sci. USA* 93:8956, incorporated by reference herein) studied the FRAG1 gene in rat osteosarcoma cells. They concluded that the FRAG1 gene product gets fused to FGF receptor 2 (FGFR2). This  
25 fusion "drastically stimulates the transforming activity and autophosphorylation of the receptor" and causes oncogenicity. Based upon sequence similarity, d24\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the d24\_1 protein sequence, centered around amino acids 34, 154, and 194 of SEQ ID NO:66,  
30 respectively.

dd24\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 24 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

5           Clone "dd426\_1"

A polynucleotide of the present invention has been identified as clone "dd426\_1". A cDNA clone was first isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
10 analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate dd426\_1 from a human adult testes (teratocarcinoma NCCIT) cDNA library. dd426\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dd426\_1 protein").

The nucleotide sequence of dd426\_1 as presently determined is reported in SEQ  
15 ID NO:67, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dd426\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:68. Amino acids 76 to 88 of SEQ ID NO:68 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 89. Due to the hydrophobic nature  
20 of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the dd426\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dd426\_1 should be approximately 800 bp.

25           The nucleotide sequence disclosed herein for dd426\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dd426\_1 demonstrated at least some similarity with sequences identified as AA760716 (nz13d06.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1287659 similar to WP:F13H10.3 CE05624 YEAST YEH4 LIKE PROTEIN;  
30 mRNA sequence), H11919 (ym10e10.r1 Homo sapiens cDNA clone 47462 5'), and Z68748 (Caenorhabditis elegans cosmid F13H10). The predicted amino acid sequence disclosed herein for dd426\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dd426\_1 protein

demonstrated at least some similarity to sequences identified as U39782 (lysine and histidine specific transporter [*Arabidopsis thaliana*]) and Z68748 (F13H10.3 [*Caenorhabditis elegans*]). Based upon sequence similarity, dd426\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the dd426\_1 protein sequence centered around amino acid 30 of SEQ ID NO:68, which may also function as a leader/signal sequence.

dd426\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 12 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "di393\_2"

A polynucleotide of the present invention has been identified as clone "di393\_2". di393\_2 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. di393\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "di393\_2 protein").

The nucleotide sequence of di393\_2 as presently determined is reported in SEQ ID NO:69, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the di393\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:70. Amino acids 7 to 19 of SEQ ID NO:70 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the di393\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone di393\_2 should be approximately 600 bp.

The nucleotide sequence disclosed herein for di393\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. di393\_2 demonstrated at least some similarity with sequences



identified as AA669506 (zu85g08.s1 Soares testis NHT Homo sapiens cDNA clone 744830 3', mRNA sequence). Based upon sequence similarity, di393\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the di393\_2 protein sequence centered around amino acid 66 of SEQ ID NO:70.

di393\_2 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 20 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### 10      Clone "dj167\_2"

A polynucleotide of the present invention has been identified as clone "dj167\_2". dj167\_2 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dj167\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dj167\_2 protein").

The nucleotide sequence of dj167\_2 as presently determined is reported in SEQ ID NO:71, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dj167\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:72.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dj167\_2 should be approximately 1550 bp.

The nucleotide sequence disclosed herein for dj167\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dj167\_2 demonstrated at least some similarity with sequences identified as H49161 (yq18d05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 274208 5'), L12350 (Human thrombospondin 2 (THBS2) mRNA, complete cds), T98917 (ye66b03.s1 Homo sapiens cDNA clone 122669 3' similar to SP:TSP1\_CHICK P35440 THROMBOSPONDIN 1), and X87620 (B.taurus mRNA for complete thrombospondin). The predicted amino acid sequence disclosed herein for dj167\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dj167\_2 protein demonstrated at least some

similarity to sequences identified as L12350 (thrombospondin 2 [Homo sapiens]), M60853 (thrombospondin [Gallus gallus]), R40823 (Human thrombospondin 1), U48245 (protein kinase C-binding protein Nel [Rattus norvegicus]), X87620 (thrombospondin [Bos taurus]), and Z71178 (B0024.14 [Caenorhabditis elegans]). Based upon sequence  
5 similarity, dj167\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the dj167\_2 protein sequence, centered around amino acids 140, 215, and 315 of SEQ ID NO:72, respectively.

10 Clone "dj167\_19"

A polynucleotide of the present invention has been identified as clone "dj167\_19". dj167\_19 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
15 analysis of the amino acid sequence of the encoded protein. dj167\_19 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dj167\_19 protein").

The nucleotide sequence of dj167\_19 as presently determined is reported in SEQ ID NO:73, and includes a poly(A) tail. What applicants presently believe to be the proper  
20 reading frame and the predicted amino acid sequence of the dj167\_19 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:74. Amino acids 22 to 34 of SEQ ID NO:74 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 35. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain  
25 should the predicted leader/signal sequence not be separated from the remainder of the dj167\_19 protein. The dj167\_19 clone is related to that of dj167\_2, and extends further 5'. The dj167\_19 clone appears to contain coding sequences for chorionic somatomammotropin in the opposite orientation at its 5' end between Sfi restriction sites (at nucleotides 16 and 839 of SEQ ID NO:73). The dj167\_2 and dj167\_19 clones may represent  
30 alternatively spliced messenger RNA molecules encoding two different forms of a secreted protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dj167\_19 should be approximately 4500 bp.

Analysis of the dj167\_19 amino acid sequence (SEQ ID NO:74) reveals the following domains: IGFBP cysteine-rich domain at amino acids 60-75; VWF-B cysteine-rich domains at amino acids 174-210, 212-247, 255-291, and 293-328; Chordin cysteine-rich domains at amino acids 336-390, 403-456, 608-662, 679-734, 753-808, and 819-873; Antistatin (protease inhibitor) cysteine-rich domains at amino acids 469-498, 505-532, 539-564, and 567-592; RGD cell attachment sequence at amino acids 314-316, and Asn glycosylation sites at amino acids 71, 113, 330, 474, and 746. The cysteine-rich domains listed above are similar to domains found in the C domain of Von Willebrand Factor (VWF), and in procollagen and thrombospondin. In addition, the amino acid sequence of SEQ ID NO:74 from amino acid 938 to amino acid 960 appears to be a transmembrane domain.

The dj167\_19 transcript is expressed in several cell types, including kidney, pancreas, spleen, and ovary, and is most abundantly expressed in placental tissue.

#### 15      Clone "dw665\_4"

A polynucleotide of the present invention has been identified as clone "dw665\_4". dw665\_4 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dw665\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dw665\_4 protein").

The nucleotide sequence of dw665\_4 as presently determined is reported in SEQ ID NO:75, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dw665\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:76. Amino acids 15 to 27 of SEQ ID NO:76 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Amino acids 16 to 28 of SEQ ID NO:76 are also a predicted leader/signal sequence, with the predicted mature amino acid sequence in that case beginning at amino acid 29. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the dw665\_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dw665\_4 should be approximately 3750 bp.

The nucleotide sequence disclosed herein for dw665\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dw665\_4 demonstrated at least some similarity with sequences identified as AA029053 (zk09f06.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 470051 3'), H77289 (EST27o17 WATM1 Homo sapiens cDNA clone 27o17, mRNA sequence), and T21722 (Human gene signature HUMGS03170). The predicted amino acid sequence disclosed herein for dw665\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dw665\_4 protein demonstrated at least some similarity to sequences identified as L35764 (chordin [Xenopus laevis]) and W31559 (Xenopus frog protein "chordin"). Analysis of motifs within the predicted dw665\_4 protein revealed the presence of Chordin cysteine-rich domains at amino acids 37-99, 115-178, and 260-322 of SEQ ID NO:76; an 'RGD' cell-attachment sequence (at amino acids 179-181 of SEQ ID NO:76), which in some proteins has been shown to play a role in cell adhesion; and Asp glycosylation sites at amino acids 118 and 291. Based upon sequence similarity, dw665\_4 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of dw665\_4 indicates that it may contain an AC repetitive element.

dw665\_4 transcripts are expressed in many tissues including kidney, adrenal gland, and prostate tissues, and are most abundantly expressed in pancreas; however, little or no dw665\_4 transcript expression is observed in liver or peripheral blood cells. dw665\_4 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 75 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis; two additional bands at approximately 26 and 30 kDa were also observed. BIAcore binding experiments indicate that dw665\_4 protein has a Chordin-like protein-binding profile, and binds to BMP-2, BMP-4, BMP-7, BMP-12, and GDF-5.

#### Clone "dx146\_12"

A polynucleotide of the present invention has been identified as clone "dx146\_12". dx146\_12 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dx146\_12 is a full-length

clone, including the entire coding sequence of a secreted protein (also referred to herein as "dx146\_12 protein").

The nucleotide sequence of dx146\_12 as presently determined is reported in SEQ ID NO:77, and includes a poly(A) tail. What applicants presently believe to be the proper  
5 reading frame and the predicted amino acid sequence of the dx146\_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:78.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dx146\_12 should be approximately 2250 bp.

The nucleotide sequence disclosed herein for dx146\_12 was searched against the  
10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dx146\_12 demonstrated at least some similarity with sequences identified as AA090429 (y0527.seq.F Fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'), AA232068 (zr24a01.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 664296 5'), AA886679 (oj47h07.s1 NCI\_CGAP\_Kid3 Homo sapiens  
15 cDNA clone IMAGE:1501501 3' similar to WP:F16A11.2 CE09424 METHANOCOCCUS HYPOTHETICAL PROTEIN 0682 LIKE; mRNA sequence), R61436 (yh15g06.r1 Homo sapiens cDNA clone 37884 5'), and Z81505 (Caenorhabditis elegans cosmid F16A11, complete sequence). The predicted amino acid sequence disclosed herein for dx146\_12 was searched against the GenPept and GeneSeq amino acid sequence  
20 databases using the BLASTX search protocol. The predicted dx146\_12 protein demonstrated at least some similarity to sequences identified as U67515 (hypothetical protein (SP P46850) [Methanococcus jannaschii]) and Z81505 (F16A11.2 [Caenorhabditis elegans]). Based upon sequence similarity, dx146\_12 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a  
25 potential transmembrane domain within the dx146\_12 protein sequence centered around amino acid 405 of SEQ ID NO:78.

dx146\_12 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 50 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

30

Clone "dx219\_13"

A polynucleotide of the present invention has been identified as clone "dx219\_13". dx219\_13 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dx219\_13 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dx219\_13 protein").

The nucleotide sequence of dx219\_13 as presently determined is reported in SEQ ID NO:79, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dx219\_13 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:80. Amino acids 94 to 106 of SEQ ID NO:80 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 107. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the dx219\_13 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dx219\_13 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for dx219\_13 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dx219\_13 demonstrated at least some similarity with sequences identified as AA429731 (zw66g05.s1 Soares testis NHT Homo sapiens cDNA clone 781208 3'), AA446067 (zw66e06.r1 Soares testis NHT Homo sapiens cDNA clone 781186 5', mRNA sequence), T23212 (standard; cDNA to mRNA; 161 BP, Human gene signature HUMGS05005), W29299 (mb99f03.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 337565 5'), W87852 (zh68b05.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 417201 5'), and Y13897 (Homo sapiens partial mRNA for hypothetical protein). Based upon sequence similarity, dx219\_13 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the dx219\_13 protein sequence, one centered around amino acid 160 and another around amino acid 275 of SEQ ID NO:80.

dx219\_13 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 37 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

5        Clone "fm3\_1"

A polynucleotide of the present invention has been identified as clone "fm3\_1". fm3\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
10 analysis of the amino acid sequence of the encoded protein. fm3\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "fm3\_1 protein").

The nucleotide sequence of fm3\_1 as presently determined is reported in SEQ ID NO:81, and includes a poly(A) tail. What applicants presently believe to be the proper  
15 reading frame and the predicted amino acid sequence of the fm3\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:82. Amino acids 7 to 19 of SEQ ID NO:82 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should  
20 the predicted leader/signal sequence not be separated from the remainder of the fm3\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fm3\_1 should be approximately 600 bp.

The nucleotide sequence disclosed herein for fm3\_1 was searched against the  
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fm3\_1 demonstrated at least some similarity with sequences identified as T15669 (IB1718 Infant brain, Bento Soares Homo sapiens cDNA 3'end). Based upon sequence similarity, fm3\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional  
30 potential transmembrane domains within the fm3\_1 protein sequence centered around amino acid 85 of SEQ ID NO:82.

fm3\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 9 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "h225\_1"

A polynucleotide of the present invention has been identified as clone "h225\_1". h225\_1 was isolated from a human adult blood (peripheral blood mononuclear cells  
5 treated with phytohemagglutinin and phorbol myristate acetate and mixed lymphocyte reaction) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. h225\_1 is a full-length clone, including the entire coding sequence  
10 of a secreted protein (also referred to herein as "h225\_1 protein").

The nucleotide sequence of h225\_1 as presently determined is reported in SEQ ID NO:83. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the h225\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:84. Amino acids 52 to 64 of SEQ ID NO:84  
15 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 65. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the h225\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
20 h225\_1 should be approximately 832 bp.

The nucleotide sequence disclosed herein for h225\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. h225\_1 demonstrated at least some similarity with sequences identified as AA604374 (no87e01.s1 NCI\_CGAP\_AA1 Homo sapiens cDNA clone  
25 IMAGE:1113816 similar to WP:ZK757.1 CE00467; mRNA sequence), H18393 (yn49a12.r1 Homo sapiens cDNA clone 171742 5' similar to SP:ZK757.1 CE00467), and R23642 (yh35e03.r1 Homo sapiens cDNA clone 131740 5'). The predicted amino acid sequence disclosed herein for h225\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted h225\_1  
30 protein demonstrated at least some similarity to sequences identified as AL022600 (hypothetical protein [Schizosaccharomyces pombe]) and Z48758 (SC9727\_21 unknown [Saccharomyces cerevisiae]). Based upon sequence similarity, h225\_1 proteins and each similar protein or peptide may share at least some activity.



Clone "kj320\_1"

A polynucleotide of the present invention has been identified as clone "kj320\_1". kj320\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. kj320\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "kj320\_1 protein").

The nucleotide sequence of kj320\_1 as presently determined is reported in SEQ ID  
10 NO:85, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the kj320\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:86. Amino acids 26 to 38 of SEQ ID NO:86 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 39. Due to the hydrophobic nature  
15 of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the kj320\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone kj320\_1 should be approximately 4900 bp.

20 The nucleotide sequence disclosed herein for kj320\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. kj320\_1 demonstrated at least some similarity with sequences identified as A45343 (Sequence 13 from Patent WO9517522), AA284111 (zc36f08.T7 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324423 3' similar to WP  
25 ZK688.8 CE00544 UDP-GALNAC; mRNA sequence), AA375707 (EST88026 HSC172 cells II Homo sapiens cDNA 5' end), AA534406 (nf76b08.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE 925815), D39885 (Rice cDNA, partial sequence (S1531\_1A)), G10010 (human STS CHLC.GCT16E06.P18287 clone GCT16E06), Q75104 (Cattle GalNAc-transferase), Q95187 (Simple tandem repeat (STR) corresponding  
30 to wg1d10), and U35890 (Rattus norvegicus polypeptide GalNAc transferase T1 mRNA, complete cds). The predicted amino acid sequence disclosed herein for kj320\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted kj320\_1 protein demonstrated at least some

similarity to sequences identified as R66397 (Cattle GalNAc-transferase), U41514 (UDP-GalNAc polypeptide N-acetylgalactosaminyltransferase [Homo sapiens]), and X85018 (UDP-GalNAc polypeptide N-acetylgalactosaminyl transferase [Homo sapiens]). Analysis of motifs within kj320\_1 reveals the presence of the alpha-2-macroglobulin family thiolester region signature. The proteinase-binding alpha-macroglobulins (A2M) are large glycoproteins found in the plasma of vertebrates, in the hemolymph of some invertebrates, and in reptilian and avian egg white. They inhibit all four classes of proteinases by trapping a proteinase with a peptide stretch containing the specific cleavage site (the 'bait' region) which upon proteinase binding induces a conformational change in the protein, trapping the proteinase. Upon cleavage of the 'bait' region, a covalent bond (a thiol-ester bond between the side chains of a cysteine and a glutamine) is formed between the A2M and the proteinase. Based upon sequence similarity, kj320\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of kj320\_1 indicates that it may contain one or more repetitive elements.

kj320\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 136 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

#### Clone "ml236\_5"

A polynucleotide of the present invention has been identified as clone "ml236\_5". ml236\_5 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ml236\_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ml236\_5 protein").

The nucleotide sequence of ml236\_5 as presently determined is reported in SEQ ID NO:87, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ml236\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:88. Amino acids 148 to 160 of SEQ ID NO:88 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 161. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a

transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ml236\_5 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ml236\_5 should be approximately 1300 bp.

5       The nucleotide sequence disclosed herein for ml236\_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ml236\_5 demonstrated at least some similarity with sequences identified as AA137204 (zl23h11.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 502821 3'), AA307966 (EST17887 Aorta endothelial cells, TNF alpha-treated Homo sapiens cDNA 5' end, mRNA sequence), AA434504 (zw31c03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770884 5' similar to WP C45G9.7 CE01858),  
10       AA525971 (ni93g09.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA clone 984448), AA526490 (ni96c11.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA clone IMAGE 984692, mRNA sequence), AF028823 (Homo sapiens Tax interaction protein 1 mRNA, partial cds), U90913 (Human clone 23665 mRNA sequence), and W73114 (zd55c12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344566 5'). The predicted amino acid sequence disclosed herein for ml236\_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ml236\_5 protein demonstrated at least some similarity to sequences identified as  
20       AF028823 (Tax interaction protein 1 [Homo sapiens]) and U21323 (similar to tight junction protein (ZO-1) (SP Z01\_HUMAN, Q07157) [Caenorhabditis elegans]). Based upon sequence similarity, ml236\_5 proteins and each similar protein or peptide may share at least some activity.

ml236\_5 protein was expressed in a COS cell expression system, and an expressed  
25       protein band of approximately 14 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "pu282\_10"

A polynucleotide of the present invention has been identified as clone "pu282\_10".  
30       pu282\_10 was isolated from a human adult blood (promyelocytic leukemia HL-60) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on

the basis of computer analysis of the amino acid sequence of the encoded protein. pu282\_10 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pu282\_10 protein").

5 The nucleotide sequence of pu282\_10 as presently determined is reported in SEQ ID NO:89, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pu282\_10 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:90. Amino acids 119 to 131 of SEQ ID NO:90 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 132. Due to the  
10 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pu282\_10 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pu282\_10 should be approximately 1050 bp.

15 The nucleotide sequence disclosed herein for pu282\_10 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pu282\_10 demonstrated at least some similarity with sequences identified as AA311503 (EST182442 Jurkat T-cells VI Homo sapiens cDNA 5' end), AA336709 (EST41341 Endometrial tumor Homo sapiens cDNA 5' end), AA336890 (EST41572 Endometrial tumor), AA385588 (EST99290 Thyroid Homo sapiens cDNA 5' end), AA526889 (ni09e05.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA clone  
20 IMAGE:967520), AC003058 (Arabidopsis thaliana "unknown" protein), and T19726 (Human gene signature HUMGS00800). Based upon sequence similarity, pu282\_10 proteins and each similar protein or peptide may share at least some activity. The  
25 TopPredII computer program predicts two additional potential transmembrane domains within the pu282\_10 protein sequence, one centered around amino acid 39 and another around amino acid 95 of SEQ ID NO:90.

pu282\_10 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 16 kDa was detected in conditioned medium  
30 and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "at94\_2"

A polynucleotide of the present invention has been identified as clone "at94\_2". at94\_2 was isolated from a human adult blood (lymphocytes and dendritic cells treated with mixed lymphocyte reaction) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as  
5 encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. at94\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "at94\_2 protein").

The nucleotide sequence of at94\_2 as presently determined is reported in SEQ ID NO:91, and includes a poly(A) tail. What applicants presently believe to be the proper  
10 reading frame and the predicted amino acid sequence of the at94\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:92. Amino acids 214 to 226 of SEQ ID NO:92 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 227. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should  
15 the predicted leader/signal sequence not be separated from the remainder of the at94\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone at94\_2 should be approximately 4300 bp.

The nucleotide sequence disclosed herein for at94\_2 was searched against the  
20 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. at94\_2 demonstrated at least some similarity with sequences identified as N24317 (yx23d12.r1 Homo sapiens cDNA clone 262583 5'), T30988 (EST25695 Homo sapiens cDNA 5' end similar to None), and U37026 (Rattus norvegicus brain sodium channel beta 2 subunit (SCNB2) mRNA, complete cds). The predicted amino  
25 acid sequence disclosed herein for at94\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted at94\_2 protein demonstrated at least some similarity to the sequence identified as Z49912 (T24F1.2 [Caenorhabditis elegans]). Based upon sequence similarity, at94\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer  
30 program predicts four additional potential transmembrane domains within the at94\_2 protein sequence, centered around amino acids 23, 306, 332, and 364 of SEQ ID NO:92, respectively.

Clone "bf169\_13"

A polynucleotide of the present invention has been identified as clone "bf169\_13". bf169\_13 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bf169\_13 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bf169\_13 protein").

The nucleotide sequence of bf169\_13 as presently determined is reported in SEQ  
10 ID NO:93, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bf169\_13 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:94. Amino acids 342 to 354 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 355. Due to the hydrophobic nature of this  
15 possible leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the bf169\_13 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bf169\_13 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for bf169\_13 was searched against the  
20 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bf169\_13 demonstrated at least some similarity with sequences identified as AA227952 (zr56b06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667379 3'), AA453914 (zx32e11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788204 5' similar to contains element TAR1 repetitive element; mRNA sequence),  
25 H46157 (yo13f11.r1 Homo sapiens cDNA clone 177837 5'), H18792 (yn52e02.r1 Homo sapiens cDNA clone 172058 5'), and N24601 (yx72e01.s1 Homo sapiens cDNA clone 267288 3'). The predicted amino acid sequence disclosed herein for bf169\_13 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bf169\_13 protein demonstrated at least some  
30 similarity to sequences identified as L41834 (plant nuclear protein [Ensis minor]) and Z75539 (F28C1.1 [Caenorhabditis elegans]). Analysis of motifs in the predicted bf169\_13 protein revealed a "mitochondrial energy transfer proteins" signature at amino acid 574 of SEQ ID NO:94. Based upon sequence similarity, bf169\_13 proteins and each similar

protein or peptide may share at least some activity. The nucleotide sequence of bf169\_13 indicates that it may contain one or more GCCCCA, GCCC, GGA and/or GC repeat sequences.

bf169\_13 protein was expressed in a COS cell expression system, and an  
 5 expressed protein band of approximately 109 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "bl152\_12"

A polynucleotide of the present invention has been identified as clone "bl152\_12".  
 10 bl152\_12 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bl152\_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein  
 15 as "bl152\_12 protein").

The nucleotide sequence of bl152\_12 as presently determined is reported in SEQ ID NO:95, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bl152\_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:96.

20 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bl152\_12 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for bl152\_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bl152\_12 demonstrated at least some similarity with sequences  
 25 identified as AA280876 (zs97d04.s1 NCI\_CGAP\_GCB1 Soares NbHTGBC Homo sapiens cDNA clone 711559 3' similar to contains element MER22 repetitive element), AA280956 (zs97d04.r1 NCI\_CGAP\_GCB1 Soares NbHTGBC Homo sapiens cDNA clone 711559 5'), R21512 (yh19b03.s1 Homo sapiens cDNA clone 130157 3'), R67018 (yi26e05.s1 Homo sapiens cDNA clone 140384 3' similar to contains MER22 repetitive element),  
 30 R71877 (yj87d11.s1 Homo sapiens cDNA clone 155733 3' similar to contains MER22 repetitive element), T22941 (Human gene signature HUMGS04666), W46539 (zc30g03.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 323860 3', mRNA sequence), and W70065 (zd49c04.s1 Soares fetal heart NbHH19W Homo sapiens cDNA

clone). The predicted amino acid sequence disclosed herein for bl152\_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bl152\_12 protein demonstrated at least some similarity to the sequence identified as Z82256 (B0513.2 [Caenorhabditis elegans]). Based upon  
5 sequence similarity, bl152\_12 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of bl152\_12 indicates that it may contain one or more GCC repeat sequences.

bl152\_12 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 25 kDa was detected in conditioned medium using SDS  
10 polyacrylamide gel electrophoresis.

#### Clone "bz578\_1"

15 A polynucleotide of the present invention has been identified as clone "bz578\_1". bz578\_1 was isolated from a human fetal kidney cDNA library using methods and was identified as encoding a novel protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bz578\_1 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "bz578\_1 protein").

20 The nucleotide sequence of bz578\_1 as presently determined is reported in SEQ ID NO:97, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bz578\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:98.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
25 bz578\_1 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for bz578\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bz578\_1 demonstrated at least some similarity with sequences identified as T47038 (yb12e08.r1 Homo sapiens cDNA clone 70982 5' contains L1  
30 repetitive element) and Z82975 (Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X). The predicted amino acid sequence disclosed herein for bz578\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bz578\_1 protein



demonstrated at least some similarity to sequences identified as AF051782 (diaphanous 1 [Homo sapiens]), U96963 (diaphanous 1 [mouse]), and U93572 (putative p150 [Homo sapiens]). Based upon sequence similarity, bz578\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of bz578\_1 indicates  
5 that it may contain one or more L1 repeat sequences.

Clone "cb123\_1"

A polynucleotide of the present invention has been identified as clone "cb123\_1". cb123\_1 was isolated from a human fetal brain cDNA library using methods which are  
10 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cb123\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cb123\_1 protein").

15 The nucleotide sequence of cb123\_1 as presently determined is reported in SEQ ID NO:99, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cb123\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:100. Amino acids 44 to 56 of SEQ ID NO:100 are a predicted leader/signal sequence, with the  
20 predicted mature amino acid sequence beginning at amino acid 57. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cb123\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
25 cb123\_1 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for cb123\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cb123\_1 demonstrated at least some similarity with sequences identified as AA309020 (EST179803 Colon carcinoma (Caco-2) cell line I Homo sapiens  
30 cDNA 5' end, mRNA sequence), R89617 (ym98b08.s1 Homo sapiens cDNA clone 166935 3'), T16814 (NIB1893 Normalized infant brain, Bento Soares Homo sapiens cDNA 3' end similar to EST02882 H. sapiens cDNA clone HFBCL71), T24092 (Human gene signature HUMGS06080), and T55187 (yb43e06.s1 Homo sapiens cDNA clone 73954 3'). The

predicted amino acid sequence disclosed herein for cb123\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cb123\_1 protein demonstrated at least some similarity to the sequence identified as U33331 (orf UL133 [Human cytomegalovirus]). Based upon sequence  
5 similarity, cb123\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the cb123\_1 protein sequence, one centered around amino acid 15 and another around amino acid 80 of SEQ ID NO:100.

10        Clone "ch245\_1"

A polynucleotide of the present invention has been identified as clone "ch245\_1". ch245\_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
15 analysis of the amino acid sequence of the encoded protein. ch245\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ch245\_1 protein").

The nucleotide sequence of ch245\_1 as presently determined is reported in SEQ ID NO:101, and includes a poly(A) tail. What applicants presently believe to be the proper  
20 reading frame and the predicted amino acid sequence of the ch245\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:102. The TopPredII computer program predicts a potential transmembrane domain within the ch245\_1 protein sequence centered around amino acid 87 of SEQ ID NO:102.

Another potential ch245\_1 reading frame and predicted amino acid sequence is  
25 encoded by basepairs 533 to 778 of SEQ ID NO:101 and is reported in SEQ ID NO:180. The TopPredII computer program predicts a potential transmembrane domain within the SEQ ID NO:180 amino acid sequence centered around amino acid 34 of SEQ ID NO:180.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ch245\_1 should be approximately 1350 bp.

30        The nucleotide sequence disclosed herein for ch245\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ch245\_1 demonstrated at least some similarity with sequences identified as AA402307 (zu48f03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA

clone 741245 5', mRNA sequence), H19032 (ym44e04.r1 Homo sapiens cDNA clone 50921 5'), H19323 (ym44e04.s1 Homo sapiens cDNA clone 50921 3'), and N36070 (yy02g11.r1 Homo sapiens cDNA clone 270116 5'). The predicted amino acid sequence disclosed herein for ch245\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ch245\_1 protein demonstrated at least some similarity to the sequence identified as M58597 (ELAM-1 ligand fucosyltransferase [Homo sapiens]) and U36763 (fatty acid synthase [Mycobacterium bovis]). Based upon sequence similarity, ch245\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "cj378\_3"

A polynucleotide of the present invention has been identified as clone "cj378\_3". cj378\_3 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cj378\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cj378\_3 protein").

The nucleotide sequence of cj378\_3 as presently determined is reported in SEQ ID NO:103, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cj378\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:104.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cj378\_3 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for cj378\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cj378\_3 demonstrated at least some similarity with sequences identified as D60138 (Human fetal brain cDNA 5'-end GEN-088A04, mRNA sequence), H19318 (ym44d06.s1 Homo sapiens cDNA clone 51231 3'), H41859 (yo07g06.r1 Homo sapiens cDNA clone 177274 5'), T25386 (Human gene signature HUMGS07551), and T75383 (yc89g05.r1 Homo sapiens cDNA clone 23351 5'). Based upon sequence

similarity, cj378\_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain at the N-terminus of the the cj378\_3 protein sequence (SEQ ID NO:104).

5           Clone "cw1481\_1"

A polynucleotide of the present invention has been identified as clone "cw1481\_1". cw1481\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
10 analysis of the amino acid sequence of the encoded protein. cw1481\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw1481\_1 protein").

The nucleotide sequence of cw1481\_1 as presently determined is reported in SEQ ID NO:105, and includes a poly(A) tail. What applicants presently believe to be the proper  
15 reading frame and the predicted amino acid sequence of the cw1481\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:106.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1481\_1 should be approximately 2380 bp.

The nucleotide sequence disclosed herein for cw1481\_1 was searched against the  
20 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw1481\_1 demonstrated at least some similarity with sequences identified as AA027927 (zk05a10.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469626 5'), AA027928 (zk05a10.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469626 3' similar to contains MER28.b2 MER28 repetitive element),  
25 AA113357 (zn69g06.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 563482 3'), AA252304 (zs12b08.s1 Soares NbHTGBC Homo sapiens cDNA clone 684951 3' similar to contains element MER22 repetitive element), AA976744 (oq09a09.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA clone IMAGE 1585816 3' similar to TR O15025 O15025 KIAA0308 ;contains element MER22 repetitive element; mRNA sequence),  
30 R55084 (yg87a06.r1 Homo sapiens cDNA clone 40244 5'), U00930 (Human clone C4E 1.63 (CAC)n/(GTG)n repeat-containing mRNA), U00955 (Human clone CE29 8.1 (CAC)n/(GTG)n repeat-containing mRNA), and W16808 (zb93a09.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320344 3'). The predicted amino acid sequence

disclosed herein for cw1481\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw1481\_1 protein demonstrated at least some similarity to sequences identified as AB002306 (KIAA0308 [Homo sapiens]), X15906 (precursor polypeptide), and Z68751 (F01G4.1 [Caenorhabditis elegans]). Based upon sequence similarity, cw1481\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the cw1481\_1 protein sequence centered around amino acid 431 of SEQ ID NO:106, and a putative transmembrane domain within the cw1481\_1 protein sequence centered around amino acid 395 of SEQ ID NO:106. The amino acid sequence of cw1481\_1 indicates that it has a histidine-rich region and a serine-rich region, and it is strongly internally repeated.

#### Clone "dd119\_4"

A polynucleotide of the present invention has been identified as clone "dd119\_4". dd119\_4 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dd119\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dd119\_4 protein").

The nucleotide sequence of dd119\_4 as presently determined is reported in SEQ ID NO:107, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dd119\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:108. Amino acids 27 to 39 of SEQ ID NO:108 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 40. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the dd119\_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dd119\_4 should be approximately 3350 bp.

The nucleotide sequence disclosed herein for dd119\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. dd119\_4 demonstrated at least some similarity with sequences identified as AA151924 (zo30e05.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 588416 5' similar to SW SLIT\_DROME P24014 SLIT PROTEIN PRECURSOR; mRNA sequence), AA193464 (zr41c06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 5 665962 3'), AB011135 (Homo sapiens mRNA for KIAA0563 protein, complete cds), G23888 (human STS WI-12393), H04996 (yl74c12.s1 Homo sapiens cDNA clone 43851 3'), M86526 (Rat proline-rich protein (PRP) gene, 5' end, and containing several Alu-like repetitive elements), M86514 (Rat proline-rich protein mRNA, 3' end), W68823 (zd37f04.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 342847 5'), and 10 Z54386 (H.sapiens CpG island DNA genomic MseI fragment, clone 10g3, forward read cpg10g3.ft1a). The predicted amino acid sequence disclosed herein for dd119\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dd119\_4 protein demonstrated at least some similarity to sequences identified as AB011135 (KIAA0563 protein [Homo sapiens]) and 15 M86526 (proline-rich protein [Rattus norvegicus]). The rat proline-rich protein (PRP) is encoded by a single-copy gene and is expressed in the ventral prostate of the rat, with the precursor protein product being cleaved into multiple proline-rich polypeptides. Based upon sequence similarity, dd119\_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential 20 transmembrane domain within the dd119\_4 protein sequence centered around amino acid 928 of SEQ ID NO:108.

dd119\_4 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 166 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "df202\_3"

A polynucleotide of the present invention has been identified as clone "df202\_3". df202\_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was 30 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. df202\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "df202\_3 protein").

The nucleotide sequence of df202\_3 as presently determined is reported in SEQ ID NO:109, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the df202\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:110.

5 Amino acids 17 to 29 of SEQ ID NO:110 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the df202\_3 protein.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone df202\_3 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for df202\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. df202\_3 demonstrated at least some similarity with sequences  
15 identified as AA138679 (mq76g03.r1 Stratagene mouse melanoma (#937312) Mus musculus cDNA clone 584692 5'), AA283121 (zt17b05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 713361 3'), AA286996 (zs58c10.r1 NCI\_CGAP\_GCB1 Soares NbHTGBC Homo sapiens cDNA clone IMAGE 701682 5'), N54968 (yv38g01.s1 Homo sapiens cDNA clone 245040 3'), T20071 (Human gene signature HUMGS01213), and  
20 W28275 (44g12 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA).

The predicted amino acid sequence disclosed herein for df202\_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted df202\_3 protein demonstrated at least some similarity to the sequence identified as Z81137 (W02D9.h [Caenorhabditis elegans]). Based upon sequence  
25 similarity, df202\_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the df202\_3 protein sequence, centered around amino acids 55, 80, and 108 of SEQ ID NO:110, respectively.

30 Clone "km225\_1"

A polynucleotide of the present invention has been identified as clone "km225\_1". km225\_1 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was

identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. km225\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "km225\_1 protein").

5       The nucleotide sequence of km225\_1 as presently determined is reported in SEQ ID NO:111, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the km225\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:112. Amino acids 9 to 21 of SEQ ID NO:112 are a predicted leader/signal sequence, with the  
10       predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the km225\_1 protein.

      The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
15       km225\_1 should be approximately 2300 bp.

      The nucleotide sequence disclosed herein for km225\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. km225\_1 demonstrated at least some similarity with sequences identified as AA101603 (zk94h09.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA  
20       clone 490529 3' similar to contains Alu repetitive element; mRNA sequence). Based upon sequence similarity, km225\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "mj301\_1"

25       A polynucleotide of the present invention has been identified as clone "mj301\_1". mj301\_1 was isolated from a human adult lymph node cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. mj301\_1 is a full-length clone,  
30       including the entire coding sequence of a secreted protein (also referred to herein as "mj301\_1 protein").

      The nucleotide sequence of mj301\_1 as presently determined is reported in SEQ ID NO:113, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the mj301\_1 protein



corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:114. Amino acids 65 to 77 of SEQ ID NO:114 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 78. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the mj301\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone mj301\_1 should be approximately 2760 bp; however, a band of 550 bp has been detected in restriction digests, possibly due to an internal EcoRI or NotI restriction site in the clone.

The nucleotide sequence disclosed herein for mj301\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. mj301\_1 demonstrated at least some similarity with sequences identified as AA053085 (zl73d01.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 510241 3'), AA347293 (EST53566 Fetal heart II Homo sapiens cDNA 5' end), AA813287 (ai76a07.s1 Soares testis NHT Homo sapiens cDNA clone 1376724 3', mRNA sequence), R45713 (Ha117-f Homo sapiens cDNA clone a117-f), T20114 (Human gene signature HUMGS01258), U46278 (Human clone xs252 mRNA sequence), Z36823 (H.sapiens (xs170) mRNA), and Z36832 (H.sapiens (xs170) mRNA). The human xs170 sequence is differentially expressed in pancreatic cancer cells. The predicted amino acid sequence disclosed herein for mj301\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted mj301\_1 protein demonstrated at least some similarity to the sequence identified as U07818 (putative phospho-beta-glucosidase [Bacillus stearothermophilus]). Based upon sequence similarity, mj301\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the mj301\_1 protein sequence centered around amino acid 60 of SEQ ID NO:114.

#### Clone "ml10\_7"

A polynucleotide of the present invention has been identified as clone "ml10\_7". ml10\_7 was isolated from a human adult brain (caudate nucleus) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis

of computer analysis of the amino acid sequence of the encoded protein. ml10\_7 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ml10\_7 protein").

5 The nucleotide sequence of ml10\_7 as presently determined is reported in SEQ ID NO:115, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ml10\_7 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:116. Amino acids 30 to 42 of SEQ ID NO:116 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 43. Due to the  
10 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ml10\_7 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ml10\_7 should be approximately 1600 bp.

15 The nucleotide sequence disclosed herein for ml10\_7 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ml10\_7 demonstrated at least some similarity with sequences identified as AA411457 (zv30f06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755171 3'), AA411585 (zv30f06.r1 Soares ovary tumor NbHOT Homo sapiens  
20 cDNA clone 755171 5', mRNA sequence), AA485512 (zx90b02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810987 5'), R97588 (yq59b05.r1 Homo sapiens cDNA clone 200049 5' similar to contains MSR1 repetitive element), and T23020 (Human gene signature HUMGS04748). The predicted amino acid sequence disclosed herein for ml10\_7 was searched against the GenPept and GeneSeq amino acid sequence databases using the  
25 BLASTX search protocol. The predicted ml10\_7 protein demonstrated at least some similarity to the sequence identified as R56978 (Human myotonic dystrophy gene protein). Based upon sequence similarity, ml10\_7 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four additional potential transmembrane domains within the ml10\_7 protein sequence, centered  
30 approximately around amino acids 20, 55 (between residues 50 and 60), 85 (between residues 80 and 89), and 175 (between residues 169 and 180) of SEQ ID NO:116, respectively. ml10\_7 appears to represent one member of a group of multiple alternatively spliced transcripts.

Clone "my340\_1"

A polynucleotide of the present invention has been identified as clone "my340\_1". my340\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. my340\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "my340\_1 protein").

The nucleotide sequence of my340\_1 as presently determined is reported in SEQ  
10 ID NO:117, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the my340\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:118.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone my340\_1 should be approximately 1800 bp.

15 The nucleotide sequence disclosed herein for my340\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. my340\_1 demonstrated at least some similarity with sequences identified as AA469015 (nc79g10.r1 NCI\_CGAP\_Pr2 Homo sapiens cDNA clone  
IMAGE:783618), H85290 (yv86f01.r1 Homo sapiens cDNA clone 249625 5'), L29074  
20 (Homo sapiens fragile X mental retardation protein (FMR-1) gene (6 alternative splices), complete cds), M86699 (Human kinase (TTK) mRNA, complete cds), W19755 (zb38f08.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 305895 5'), W63667 (zc57h10.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 326467 5', mRNA sequence), and Z84478 (Human DNA sequence). The predicted amino  
25 acid sequence disclosed herein for my340\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted my340\_1 protein demonstrated at least some similarity to the sequence identified as M86699 (kinase [Homo sapiens]). The human TTK kinase can phosphorylate serine, threonine, and tyrosine hydroxyamino acids. Based upon sequence similarity,  
30 my340\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the my340\_1 protein sequence centered around amino acid 50 of SEQ ID NO:28.

Deposit of Clones

Clones bn365\_53, bo342\_2, dn721\_8, dn834\_1, pd278\_5, pe80\_1, pm113\_1, pm749\_8, pt31\_4, and pv296\_5 were deposited on May 7, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.)  
5 as an original deposit under the Budapest Treaty and were given the accession number ATCC 98752, from which each clone comprising a particular polynucleotide is obtainable.

Clones er311\_20, fh149\_12, pc201\_6, pl87\_1, and pm514\_4 were deposited on June 2, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty  
10 and were given the accession number ATCC 98781, from which each clone comprising a particular polynucleotide is obtainable.

Clones co155\_12, fn189\_13, lv2\_47, ml243\_1, pm96\_9, pu261\_1, pw214\_15, qb56\_19, qc646\_1, qf116\_2, and qf662\_3 were deposited on July 2, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209  
15 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98808, from which each clone comprising a particular polynucleotide is obtainable.

Clones am748\_5, cj507\_1, cn922\_5, cw691\_11, cw1000\_2, cw1640\_1, d24\_1, dd426\_1, and di393\_2 were deposited on July 16, 1998 with the American Type Culture  
20 Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98817, from which each clone comprising a particular polynucleotide is obtainable.

Clones dj167\_2, dw665\_4, dx146\_12, dx219\_13, fm3\_1, h225\_1, kj320\_1, ml236\_5, and pu282\_10, were deposited on July 16, 1998 with the American Type Culture  
25 Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98818, from which each clone comprising a particular polynucleotide is obtainable.

Clones at94\_2, bf169\_13, bl152\_12, bz578\_1, cb123\_1, ch245\_1, cj378\_3, cw1481\_1, dd119\_4, df202\_3, km225\_1, mj301\_1, ml10\_7, and my340\_1 were deposited on July 22,  
30 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98822, from which each clone comprising a particular polynucleotide is obtainable.

Clone dj167\_19 was deposited on February 5, 1999 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number ATCC 207090, from which the dj167\_19 clone comprising a particular polynucleotide is obtainable.

All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

Each clone has been transfected into separate bacterial cells (*E. coli*) in the composite deposits above. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Figures 1A and 1B, respectively. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* 19: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* 9: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

Clone

bn365\_53

Probe Sequence

SEQ ID NO:119

	bo342_2	SEQ ID NO:120
	dn721_8	SEQ ID NO:121
	dn834_1	SEQ ID NO:122
	pd278_5	SEQ ID NO:123
5	pe80_1	SEQ ID NO:124
	pm113_1	SEQ ID NO:125
	pm749_8	SEQ ID NO:126
	pt31_4	SEQ ID NO:127
	pv296_5	SEQ ID NO:128
10	er311_20	SEQ ID NO:129
	fh149_12	SEQ ID NO:130
	pc201_6	SEQ ID NO:131
	pl87_1	SEQ ID NO:132
	pm514_4	SEQ ID NO:133
15	co155_12	SEQ ID NO:134
	fn189_13	SEQ ID NO:135
	lv2_47	SEQ ID NO:136
	ml243_1	SEQ ID NO:137
	pm96_9	SEQ ID NO:138
20	pu261_1	SEQ ID NO:139
	pw214_15	SEQ ID NO:140
	qb56_19	SEQ ID NO:141
	qc646_1	SEQ ID NO:142
	qf116_2	SEQ ID NO:143
25	qf662_3	SEQ ID NO:144
	am748_5	SEQ ID NO:145
	cj507_1	SEQ ID NO:146
	cn922_5	SEQ ID NO:147
	cw691_11	SEQ ID NO:148
30	cw1000_2	SEQ ID NO:149
	cw1640_1	SEQ ID NO:150
	d24_1	SEQ ID NO:151
	dd426_1	SEQ ID NO:152
	di393_2	SEQ ID NO:153

	dj167_2	SEQ ID NO:154
	dw665_4	SEQ ID NO:155
	dx146_12	SEQ ID NO:156
	dx219_13	SEQ ID NO:157
5	fm3_1	SEQ ID NO:158
	h225_1	SEQ ID NO:159
	kj320_1	SEQ ID NO:160
	ml236_5	SEQ ID NO:161
	pu282_10	SEQ ID NO:162
10	at94_2	SEQ ID NO:163
	bf169_13	SEQ ID NO:164
	bl152_12	SEQ ID NO:165
	bz578_1	SEQ ID NO:166
	cb123_1	SEQ ID NO:167
15	ch245_1	SEQ ID NO:168
	cj378_3	SEQ ID NO:169
	cw1481_1	SEQ ID NO:170
	dd119_4	SEQ ID NO:171
	df202_3	SEQ ID NO:172
20	km225_1	SEQ ID NO:173
	mj301_1	SEQ ID NO:174
	ml10_7	SEQ ID NO:175
	my340_1	SEQ ID NO:176

25 In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

30 The design of the oligonucleotide probe should preferably follow these parameters:

- (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;

- (b) It should be designed to have a  $T_m$  of approx. 80 ° C (assuming 2° for each A or T and 4 degrees for each G or C).

The oligonucleotide should preferably be labeled with  $\gamma$ -<sup>32</sup>P ATP (specific activity 6000 Ci/mmmole) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4e+6 dpm/pmmole.

- 10 The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 µl of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100 µg/ml. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the  
15 dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 µg/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

- Standard colony hybridization procedures should then be used to transfer the  
20 colonies to nitrocellulose filters and lyse, denature and bake them.

- The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 µg/ml of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at  
25 a concentration greater than or equal to 1e+6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The  
30 filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.



The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

5 Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as  
10 immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a  
15 decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein may be obtained by expression of the disclosed full-length  
20 polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that  
25 are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can  
30 be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that

has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately  
5 labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible to determine the corresponding chromosomal location for a disclosed polynucleotide by identifying significantly similar nucleotide sequences in public databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences  
10 disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession number. Searches using the GenBank accession numbers of these public database sequences can then be performed at an Internet site provided by the National Center for Biotechnology Information having the address <http://www.ncbi.nlm.nih.gov/UniGene/>, in order to  
15 identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters" so identified will already have been mapped to particular chromosomal sites.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense  
20 polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* 15(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* 62(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed  
25 herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein).  
30 In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of

transposable elements (Plasterk, 1992, *Bioessays* 14(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of transmembrane domains in an amino acid sequence, domains which are described by the location of the center of the transmembrane domain, with at least ten transmembrane amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST

version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle *ed.*, *Methods in Enzymology* **266**: 460-480; Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of Molecular Biology* **215**: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, *Nature Genetics* **3**: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci. USA* **90**: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX platforms can be downloaded from <ftp://blast.wustl.edu/blast/executables>. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely used for commercial, nonprofit, or academic purposes. In all search programs in the suite -- BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length one is Q=9 for proteins and BLASTP, and Q=10 for BLASTN, but may be changed to any integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. Any combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps. The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or

polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus*, *Hylobates concolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, *Aotus trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*, *Cricetulus griseus*, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species (O'Brien and Seuánez, 1988, *Ann. Rev. Genet.* 22: 323-351; O'Brien *et al.*, 1993, *Nature Genetics* 3:103-112; Johansson *et al.*, 1995, *Genomics* 25: 682-690; Lyons *et al.*, 1997, *Nature Genetics* 15: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* 13(10): 393-399; Carver and Stubbs, 1997, *Genome Research* 7:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

5 The present invention also includes polynucleotides that hybridize under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) <sup>‡</sup>	Hybridization Temperature and Buffer <sup>†</sup>	Wash Temperature and Buffer <sup>†</sup>
A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
B	DNA:DNA	<50	T <sub>B</sub> <sup>*</sup> ; 1xSSC	T <sub>B</sub> <sup>*</sup> ; 1xSSC
C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
D	DNA:RNA	<50	T <sub>D</sub> <sup>*</sup> ; 1xSSC	T <sub>D</sub> <sup>*</sup> ; 1xSSC
E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
F	RNA:RNA	<50	T <sub>F</sub> <sup>*</sup> ; 1xSSC	T <sub>F</sub> <sup>*</sup> ; 1xSSC
G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
H	DNA:DNA	<50	T <sub>H</sub> <sup>*</sup> ; 4xSSC	T <sub>H</sub> <sup>*</sup> ; 4xSSC
I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
J	DNA:RNA	<50	T <sub>J</sub> <sup>*</sup> ; 4xSSC	T <sub>J</sub> <sup>*</sup> ; 4xSSC
K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
L	RNA:RNA	<50	T <sub>L</sub> <sup>*</sup> ; 2xSSC	T <sub>L</sub> <sup>*</sup> ; 2xSSC
M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
N	DNA:DNA	<50	T <sub>N</sub> <sup>*</sup> ; 6xSSC	T <sub>N</sub> <sup>*</sup> ; 6xSSC
O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
P	DNA:RNA	<50	T <sub>P</sub> <sup>*</sup> ; 6xSSC	T <sub>P</sub> <sup>*</sup> ; 6xSSC
Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
R	RNA:RNA	<50	T <sub>R</sub> <sup>*</sup> ; 4xSSC	T <sub>R</sub> <sup>*</sup> ; 4xSSC

<sup>‡</sup>: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

<sup>†</sup>: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH<sub>2</sub>PO<sub>4</sub>, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

<sup>\*</sup>T<sub>B</sub> - T<sub>R</sub>: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T<sub>m</sub>) of the hybrid, where T<sub>m</sub> is determined according to the following equations. For hybrids less than 18 base pairs in length, T<sub>m</sub>(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T<sub>m</sub>(°C) = 81.5 + 16.6(log<sub>10</sub>[Na<sup>+</sup>]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na<sup>+</sup>] is the concentration of sodium ions in the hybridization buffer ([Na<sup>+</sup>] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds.,  
5 John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or  
10 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide of the invention may be operably linked to an  
15 expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably  
20 linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the  
25 protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

30 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial



strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art

given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

### USES AND BIOLOGICAL ACTIVITY

5       The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies  
10       or vectors suitable for introduction of DNA).

#### Research Uses and Utilities

      The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express  
15       recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare  
20       with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for  
25       examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those  
30       described in Gyuris *et al.*, 1993, *Cell* 75: 791-803 and in Rossi *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* 94: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine  
5 levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the  
10 protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent  
15 grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to  
20 Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

#### Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein  
25 or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention  
30 can be added to the medium in or on which the microorganism is cultured.

#### Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may

induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

- 10 Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

- 20 Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon  $\gamma$ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

- 25 Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., *Proc. Natl. Acad. Sci. U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991;

Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease.

Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term

tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

5       The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as  
10       described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

15       Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms.  
20       Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from  
25       the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/*lpr/lpr* mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and  
30       murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune



response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$

microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated  
 5 immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated  
 10 immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without  
 15 limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al.,  
 20 J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnoli et al.,  
 25 Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro*  
 30 antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek,

D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

- 5 Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995;
- 10 Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

- Assays for lymphocyte survival/apoptosis (which will identify, among others,
- 15 proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993;
- 20 Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

- Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

25

#### Hematopoiesis Regulating Activity

- A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell
- 30 lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid

cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al., *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and

Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

5

#### Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns,  
10 incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as  
15 well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal  
20 disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue  
25 destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in  
30 circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and

in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation

of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

5 A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

10 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium ).

15 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

#### 20 Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- $\beta$  group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

#### Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. *J. Clin. Invest.* 95:1370-1376, 1995; Lind et al.



APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

#### Hemostatic and Thrombolytic Activity

5 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting  
10 formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

15 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

#### 20 Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands,  
25 receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant  
30 receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160, 1989; Stoltenberg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

#### 10        Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

25

#### Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

30

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved

extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this  
5 recognition site can change the specificity of a cadherin so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells  
10 become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas  
15 to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed  
20 in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the  
25 inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block  
30 the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

#### Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

#### Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s);

effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic  
5 lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another  
10 material or entity which is cross-reactive with such protein.

### **ADMINISTRATION AND DOSING**

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a  
15 pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the  
20 carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other  
25 agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor,  
30 thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical

compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in  
5 combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If  
10 administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical  
15 composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is  
20 administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention.  
25 When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid  
30 form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present

invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

10 The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1mg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein of the present invention per kg body weight.

20 The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the term "antibody" includes without limitation a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted antibody, a humanized antibody, or fragments thereof which bind to the indicated protein.



Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of  
5 antibody-producing hybridomas in accordance with known methods (see for example, Goding, 1983, *Monoclonal antibodies: principles and practice*, Academic Press Inc., New York; and Yokoyama, 1992, "Production of Monoclonal Antibodies" in *Current Protocols in Immunology*, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the  
10 relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, *supra*; and Andrew et al., 1992, "Fragmentation of Immunoglobulins" in *Current Protocols in Immunology*, Unit 2.8, Greene Publishing  
15 Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for example, U.S. Patent Nos. 5,530,101, 5,585,089, and 5,693,762). Additionally, human antibodies may be  
20 produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild *et al.*, 1996, *Nature Biotechnology* 14: 845-851; Mendez *et al.*, 1997, *Nature Genetics* 15: 146-156 (erratum *Nature Genetics* 16: 410); and U.S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide  
25 immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful  
30 diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where

abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

5 For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably  
10 be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the  
15 methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical  
20 applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium  
25 sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other  
30 ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions  
5 from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-  
10 methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to  
15 provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in  
20 question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to  
25 humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of  
30 a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect

the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

5 Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

10 Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
  - (a) the nucleotide sequence of SEQ ID NO:1;
  - (b) the nucleotide sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366;
  - (c) the nucleotide sequence of the full-length protein coding sequence of clone bn365\_53 deposited under accession number ATCC 98752;
  - (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone bn365\_53 deposited under accession number ATCC 98752;
  - (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
  - (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;
  - (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
  - (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:1.
2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.
3. A host cell transformed with the polynucleotide of claim 2.
4. The host cell of claim 3, wherein said cell is a mammalian cell.
5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:

- (a) growing a culture of a host cell transformed with the polynucleotide of claim 2 in a suitable culture medium; and
  - (b) purifying said protein from the culture.
- 6. A protein produced according to the process of claim 5.
- 7. An isolated polynucleotide encoding the protein of claim 6.
- 8. The polynucleotide of claim 7, wherein the polynucleotide comprises the cDNA insert of clone bn365\_53 deposited under accession number ATCC 98752.
- 9. A protein comprising an amino acid sequence selected from the group consisting of:
  - (a) the amino acid sequence of SEQ ID NO:2;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone bn365\_53 deposited under accession number ATCC 98752;the protein being substantially free from other mammalian proteins.
- 10. The protein of claim 9, wherein said protein comprises the amino acid sequence of SEQ ID NO:2.
- 11. A composition comprising the protein of claim 9 and a pharmaceutically acceptable carrier.
- 12. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
  - (a) the nucleotide sequence of SEQ ID NO:3;
  - (b) the nucleotide sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915;
  - (c) the nucleotide sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915;

- (d) the nucleotide sequence of the full-length protein coding sequence of clone bo342\_2 deposited under accession number ATCC 98752;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;
- (f) the nucleotide sequence of a mature protein coding sequence of clone bo342\_2 deposited under accession number ATCC 98752;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:4;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:3.

13. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:4;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;
- the protein being substantially free from other mammalian proteins.

14. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:5;

(b) the nucleotide sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689;

(c) the nucleotide sequence of the full-length protein coding sequence of clone dn721\_8 deposited under accession number ATCC 98752;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:6;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:5.

15. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:6;

(b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and

(c) the amino acid sequence encoded by the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins.

16. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:7;

(b) the nucleotide sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484;



- (c) the nucleotide sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone dn834\_1 deposited under accession number ATCC 98752;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752;
- (f) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (g) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(e); and
- (i) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(e), and that has a length that is at least 25% of the length of SEQ ID NO:7.

17. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
- (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins.

18. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:9;
- (b) the nucleotide sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420;

(c) the nucleotide sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420;

(d) the nucleotide sequence of the full-length protein coding sequence of clone pd278\_5 deposited under accession number ATCC 98752;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;

(f) the nucleotide sequence of a mature protein coding sequence of clone pd278\_5 deposited under accession number ATCC 98752;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:9.

19. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:10;

(b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and

(c) the amino acid sequence encoded by the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins.

20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:11;
- (b) the nucleotide sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pe80\_1 deposited under accession number ATCC 98752;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:12;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:11.

21. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752;
- the protein being substantially free from other mammalian proteins.

22. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:13;

- (b) the nucleotide sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428;
- (c) the nucleotide sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone pm113\_1 deposited under accession number ATCC 98752;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;
- (f) the nucleotide sequence of a mature protein coding sequence of clone pm113\_1 deposited under accession number ATCC 98752;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:14;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:13.

23. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
- (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins.

24. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:15;
- (b) the nucleotide sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pm749\_8 deposited under accession number ATCC 98752;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pm749\_8 deposited under accession number ATCC 98752;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:15.

25. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pm749\_8 deposited under accession number ATCC 98752;
- the protein being substantially free from other mammalian proteins.

26. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:17;
- (b) the nucleotide sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023;
- (c) the nucleotide sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone pt31\_4 deposited under accession number ATCC 98752;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;
- (f) the nucleotide sequence of a mature protein coding sequence of clone pt31\_4 deposited under accession number ATCC 98752;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:18;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:17.

27. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:18;
- (b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and

(c) the amino acid sequence encoded by the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752; the protein being substantially free from other mammalian proteins.

28. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:19;
- (b) the nucleotide sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pv296\_5 deposited under accession number ATCC 98752;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:19.

29. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:20;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752;
- the protein being substantially free from other mammalian proteins.

30. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:21;
- (b) the nucleotide sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone er311\_20 deposited under accession number ATCC 98781;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:21.

31. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:22;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;
- the protein being substantially free from other mammalian proteins.



32. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:23;
- (b) the nucleotide sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043;
- (c) the nucleotide sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone fh149\_12 deposited under accession number ATCC 98781;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;
- (f) the nucleotide sequence of a mature protein coding sequence of clone fh149\_12 deposited under accession number ATCC 98781;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:24;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:23.

33. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:24;
- (b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and

(c) the amino acid sequence encoded by the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781; the protein being substantially free from other mammalian proteins.

34. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:25;
- (b) the nucleotide sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099;
- (c) the nucleotide sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone pc201\_6 deposited under accession number ATCC 98781;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;
- (f) the nucleotide sequence of a mature protein coding sequence of clone pc201\_6 deposited under accession number ATCC 98781;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:26;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:25.

35. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:26;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;
- the protein being substantially free from other mammalian proteins.

36. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:27;
- (b) the nucleotide sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pl87\_1 deposited under accession number ATCC 98781;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pl87\_1 deposited under accession number ATCC 98781;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:27.

37. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:28;
- (b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and

(c) the amino acid sequence encoded by the cDNA insert of clone pl87\_1 deposited under accession number ATCC 98781; the protein being substantially free from other mammalian proteins.

38. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:29;
- (b) the nucleotide sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pm514\_4 deposited under accession number ATCC 98781;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:30;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:29.

39. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;
- (b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;

the protein being substantially free from other mammalian proteins.

40. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:31;
- (b) the nucleotide sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997;
- (c) the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone co155\_12 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;
- (f) the nucleotide sequence of a mature protein coding sequence of clone co155\_12 deposited under accession number ATCC 98808;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:32;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:31.

41. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:32;

- (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

42. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:33;
- (b) the nucleotide sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343;
- (c) the nucleotide sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone fn189\_13 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;
- (f) the nucleotide sequence of a mature protein coding sequence of clone fn189\_13 deposited under accession number ATCC 98808;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:34;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:33.

43. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:34;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

44. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:35;
- (b) the nucleotide sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide 557;
- (c) the nucleotide sequence of SEQ ID NO:35 from nucleotide 235 to nucleotide 899;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone lv2\_47 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone lv2\_47 deposited under accession number ATCC 98808;
- (f) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:36;
- (g) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36;
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(e); and
- (i) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(e), and that has a length that is at least 25% of the length of SEQ ID NO:35.

45. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:36;
- (b) the amino acid sequence of SEQ ID NO:36 from amino acid 58 to amino acid 164;
- (c) a fragment of the amino acid sequence of SEQ ID NO:36, the fragment comprising eight contiguous amino acids of SEQ ID NO:36; and
- (d) the amino acid sequence encoded by the cDNA insert of clone lv2\_47 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins.

46. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:37;
- (b) the nucleotide sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499;
- (c) the nucleotide sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ml243\_1 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ml243\_1 deposited under accession number ATCC 98808;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:38;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and



(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:37.

47. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:38;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

48. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:39;
- (b) the nucleotide sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pm96\_9 deposited under accession number ATCC 98808;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:39.

49. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

50. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:41;
- (b) the nucleotide sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762;
- (c) the nucleotide sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone pu261\_1 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;
- (f) the nucleotide sequence of a mature protein coding sequence of clone pu261\_1 deposited under accession number ATCC 98808;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:41.

51. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:42;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

52. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:43;
- (b) the nucleotide sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone pw214\_15 deposited under accession number ATCC 98808;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:44;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;

- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:43.

53. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:44;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

54. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:45;
- (b) the nucleotide sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone qb56\_19 deposited under accession number ATCC 98808;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:46;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:45.

55. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:46;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

56. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:47;
- (b) the nucleotide sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273;
- (c) the nucleotide sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone qc646\_1 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;
- (f) the nucleotide sequence of a mature protein coding sequence of clone qc646\_1 deposited under accession number ATCC 98808;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:48;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:47.

57. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

58. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:49;
- (b) the nucleotide sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone qf116\_2 deposited under accession number ATCC 98808;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:50;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:49.

59. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:50;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

60. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:51;
- (b) the nucleotide sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741;
- (c) the nucleotide sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone qf662\_3 deposited under accession number ATCC 98808;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808;
- (f) the nucleotide sequence of a mature protein coding sequence of clone qf662\_3 deposited under accession number ATCC 98808;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:52;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:51.

61. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:52;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins.

62. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:53;
- (b) the nucleotide sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196;
- (c) the nucleotide sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone am748\_5 deposited under accession number ATCC 98817;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;
- (f) the nucleotide sequence of a mature protein coding sequence of clone am748\_5 deposited under accession number ATCC 98817;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;



(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:54;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:53.

63. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:54;

(b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and

(c) the amino acid sequence encoded by the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins.

64. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:55;

(b) the nucleotide sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310;

(c) the nucleotide sequence of the full-length protein coding sequence of clone cj507\_1 deposited under accession number ATCC 98817;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:56;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:55.

65. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:56;

(b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and

(c) the amino acid sequence encoded by the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins.

66. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:57;

(b) the nucleotide sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328;

(c) the nucleotide sequence of the full-length protein coding sequence of clone cn922\_5 deposited under accession number ATCC 98817;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:58;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:57.

67. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:58;

(b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and

(c) the amino acid sequence encoded by the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins.

68. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:59;

(b) the nucleotide sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942;

(c) the nucleotide sequence of the full-length protein coding sequence of clone cw691\_11 deposited under accession number ATCC 98817;

(d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817;

(e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:60;

(f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:59.

69. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:60;

(b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and

(c) the amino acid sequence encoded by the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins.

70. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:61;

(b) the nucleotide sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252;

(c) the nucleotide sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252;

(d) the nucleotide sequence of the full-length protein coding sequence of clone cw1000\_2 deposited under accession number ATCC 98817;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;

(f) the nucleotide sequence of a mature protein coding sequence of clone cw1000\_2 deposited under accession number ATCC 98817;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:62;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:61.

71. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:62;

(b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and

(c) the amino acid sequence encoded by the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins.

72. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:63;

(b) the nucleotide sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296;

(c) the nucleotide sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296;

(d) the nucleotide sequence of the full-length protein coding sequence of clone cw1640\_1 deposited under accession number ATCC 98817;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;

- (f) the nucleotide sequence of a mature protein coding sequence of clone cw1640\_1 deposited under accession number ATCC 98817;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:64;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:63.

73. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:64;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;
- the protein being substantially free from other mammalian proteins.

74. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:65;
- (b) the nucleotide sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827;
- (c) the nucleotide sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827;

- (d) the nucleotide sequence of the full-length protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;
- (f) the nucleotide sequence of a mature protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:66;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:65.

75. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:66;
- (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
- (c) the amino acid sequence encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins.

76. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:67;

- (b) the nucleotide sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529;
- (c) the nucleotide sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone dd426\_1 deposited under accession number ATCC 98817;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817;
- (f) the nucleotide sequence of a mature protein coding sequence of clone dd426\_1 deposited under accession number ATCC 98817;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:68;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:67.

77. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:68;
- (b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins.



78. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:69;
- (b) the nucleotide sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543;
- (c) the nucleotide sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone di393\_2 deposited under accession number ATCC 98817;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone di393\_2 deposited under accession number ATCC 98817;
- (f) the nucleotide sequence of a mature protein coding sequence of clone di393\_2 deposited under accession number ATCC 98817;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone di393\_2 deposited under accession number ATCC 98817;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:70;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:69.

79. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:70;
- (b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and

(c) the amino acid sequence encoded by the cDNA insert of clone di393\_2 deposited under accession number ATCC 98817; the protein being substantially free from other mammalian proteins.

80. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:71;
- (b) the nucleotide sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone dj167\_2 deposited under accession number ATCC 98818;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:72;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:71.

81. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:72;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818;
- the protein being substantially free from other mammalian proteins.

82. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:73;
- (b) the nucleotide sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490;
- (c) the nucleotide sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490;
- (d) the nucleotide sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343;
- (e) the nucleotide sequence of the full-length protein coding sequence of clone dj167\_19 deposited under accession number ATCC 207090;
- (f) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090;
- (g) the nucleotide sequence of a mature protein coding sequence of clone dj167\_19 deposited under accession number ATCC 207090;
- (h) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090;
- (i) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:74;
- (j) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h); and
- (l) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h), and that has a length that is at least 25% of the length of SEQ ID NO:73.

83. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:74;

- (b) the amino acid sequence of SEQ ID NO:74 from amino acid 637 to amino acid 1036;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090;
- the protein being substantially free from other mammalian proteins.

84. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:75;
- (b) the nucleotide sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441;
- (c) the nucleotide sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone dw665\_4 deposited under accession number ATCC 98818;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;
- (f) the nucleotide sequence of a mature protein coding sequence of clone dw665\_4 deposited under accession number ATCC 98818;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:76;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees

C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:75.

85. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:76;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;
- the protein being substantially free from other mammalian proteins.

86. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:77;
- (b) the nucleotide sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone dx146\_12 deposited under accession number ATCC 98818;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:78;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:77.

87. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818;
- the protein being substantially free from other mammalian proteins.

88. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:79;
- (b) the nucleotide sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948;
- (c) the nucleotide sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone dx219\_13 deposited under accession number ATCC 98818;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;
- (f) the nucleotide sequence of a mature protein coding sequence of clone dx219\_13 deposited under accession number ATCC 98818;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:80;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:79.

89. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:80;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;
- the protein being substantially free from other mammalian proteins.

90. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:81;
- (b) the nucleotide sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286;
- (c) the nucleotide sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone fm3\_1 deposited under accession number ATCC 98818;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;
- (f) the nucleotide sequence of a mature protein coding sequence of clone fm3\_1 deposited under accession number ATCC 98818;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:82;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:81.

91. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:82;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;
- the protein being substantially free from other mammalian proteins.

92. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:83;
- (b) the nucleotide sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572;
- (c) the nucleotide sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone h225\_1 deposited under accession number ATCC 98818;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;
- (f) the nucleotide sequence of a mature protein coding sequence of clone h225\_1 deposited under accession number ATCC 98818;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:84;



(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:83.

93. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:84;

(b) a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84; and

(c) the amino acid sequence encoded by the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins.

94. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:85;

(b) the nucleotide sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210;

(c) the nucleotide sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210;

(d) the nucleotide sequence of the full-length protein coding sequence of clone kj320\_1 deposited under accession number ATCC 98818;

(e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;

(f) the nucleotide sequence of a mature protein coding sequence of clone kj320\_1 deposited under accession number ATCC 98818;

(g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;

(h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:86;

(i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86;

(j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:85.

95. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:86;

(b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and

(c) the amino acid sequence encoded by the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins.

96. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:87;

(b) the nucleotide sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899;

(c) the nucleotide sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899;

(d) the nucleotide sequence of the full-length protein coding sequence of clone ml236\_5 deposited under accession number ATCC 98818;

- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ml236\_5 deposited under accession number ATCC 98818;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:88;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:87.

97. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:88;
- (b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins.

98. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:89;
- (b) the nucleotide sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452;

- (c) the nucleotide sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone pu282\_10 deposited under accession number ATCC 98818;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;
- (f) the nucleotide sequence of a mature protein coding sequence of clone pu282\_10 deposited under accession number ATCC 98818;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:90;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:89.

99. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:90;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;
- the protein being substantially free from other mammalian proteins.

100. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:91;
- (b) the nucleotide sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179;
- (c) the nucleotide sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone at94\_2 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;
- (f) the nucleotide sequence of a mature protein coding sequence of clone at94\_2 deposited under accession number ATCC 98822;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:92;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:91.

101. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:92;
- (b) a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92; and

(c) the amino acid sequence encoded by the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822; the protein being substantially free from other mammalian proteins.

102. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:93;
- (b) the nucleotide sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone bf169\_13 deposited under accession number ATCC 98822;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:94;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:93.

103. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:94;
- (b) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and
- (c) the amino acid sequence encoded by the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins.

104. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:95;
- (b) the nucleotide sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone bl152\_12 deposited under accession number ATCC 98822;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:96;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:95.

105. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:96;
- (b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and
- (c) the amino acid sequence encoded by the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins.

106. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:97;
- (b) the nucleotide sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone bz578\_1 deposited under accession number ATCC 98822;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:98;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:97.

107. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:98;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins.

108. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:99;



- (b) the nucleotide sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992;
- (c) the nucleotide sequence of SEQ ID NO:99 from nucleotide 765 to nucleotide 992;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone cb123\_1 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822;
- (f) the nucleotide sequence of a mature protein coding sequence of clone cb123\_1 deposited under accession number ATCC 98822;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:100;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:99.

109. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:100;
- (b) a fragment of the amino acid sequence of SEQ ID NO:100, the fragment comprising eight contiguous amino acids of SEQ ID NO:100; and
- (c) the amino acid sequence encoded by the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins.

110. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:101;
- (b) the nucleotide sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone ch245\_1 deposited under accession number ATCC 98822;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:102;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:101.

111. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:102;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins.

112. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:103;

- (b) the nucleotide sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone cj378\_3 deposited under accession number ATCC 98822;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:104;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;
- (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:103.

113. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:104;
- (b) a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104; and
- (c) the amino acid sequence encoded by the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins.

114. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:105;
- (b) the nucleotide sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202;

- (c) the nucleotide sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone cw1481\_1 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;
- (f) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:106;
- (g) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;
- (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(e); and
- (i) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(e), and that has a length that is at least 25% of the length of SEQ ID NO:105.

115. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:106;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins.

116. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:107;
- (b) the nucleotide sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905;

- (c) the nucleotide sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone dd119\_4 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;
- (f) the nucleotide sequence of a mature protein coding sequence of clone dd119\_4 deposited under accession number ATCC 98822;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:108;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:107.

117. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:108;
- (b) a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins.

118. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:109;
- (b) the nucleotide sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369;
- (c) the nucleotide sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone df202\_3 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;
- (f) the nucleotide sequence of a mature protein coding sequence of clone df202\_3 deposited under accession number ATCC 98822;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:110;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:109.

119. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:110;
- (b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and

(c) the amino acid sequence encoded by the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822; the protein being substantially free from other mammalian proteins.

120. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:111;
- (b) the nucleotide sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539;
- (c) the nucleotide sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone km225\_1 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822;
- (f) the nucleotide sequence of a mature protein coding sequence of clone km225\_1 deposited under accession number ATCC 98822;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:112;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:111.

121. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:112;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins.

122. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:113;
- (b) the nucleotide sequence of SEQ ID NO:113 from nucleotide 1734 to nucleotide 2030;
- (c) the nucleotide sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone mj301\_1 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;
- (f) the nucleotide sequence of a mature protein coding sequence of clone mj301\_1 deposited under accession number ATCC 98822;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:114;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees



C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:113.

123. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:114;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:114, the fragment comprising eight contiguous amino acids of SEQ ID NO:114; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins.

124. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:115;
- (b) the nucleotide sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350;
- (c) the nucleotide sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350;
- (d) the nucleotide sequence of the full-length protein coding sequence of clone ml10\_7 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;
- (f) the nucleotide sequence of a mature protein coding sequence of clone ml10\_7 deposited under accession number ATCC 98822;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:116;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;

- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:115.

125. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:116;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins.

126. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:117;
- (b) the nucleotide sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094;
- (c) the nucleotide sequence of the full-length protein coding sequence of clone my340\_1 deposited under accession number ATCC 98822;
- (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822;
- (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:118;
- (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;

(g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and

(h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:117.

127. A protein comprising an amino acid sequence selected from the group consisting of:

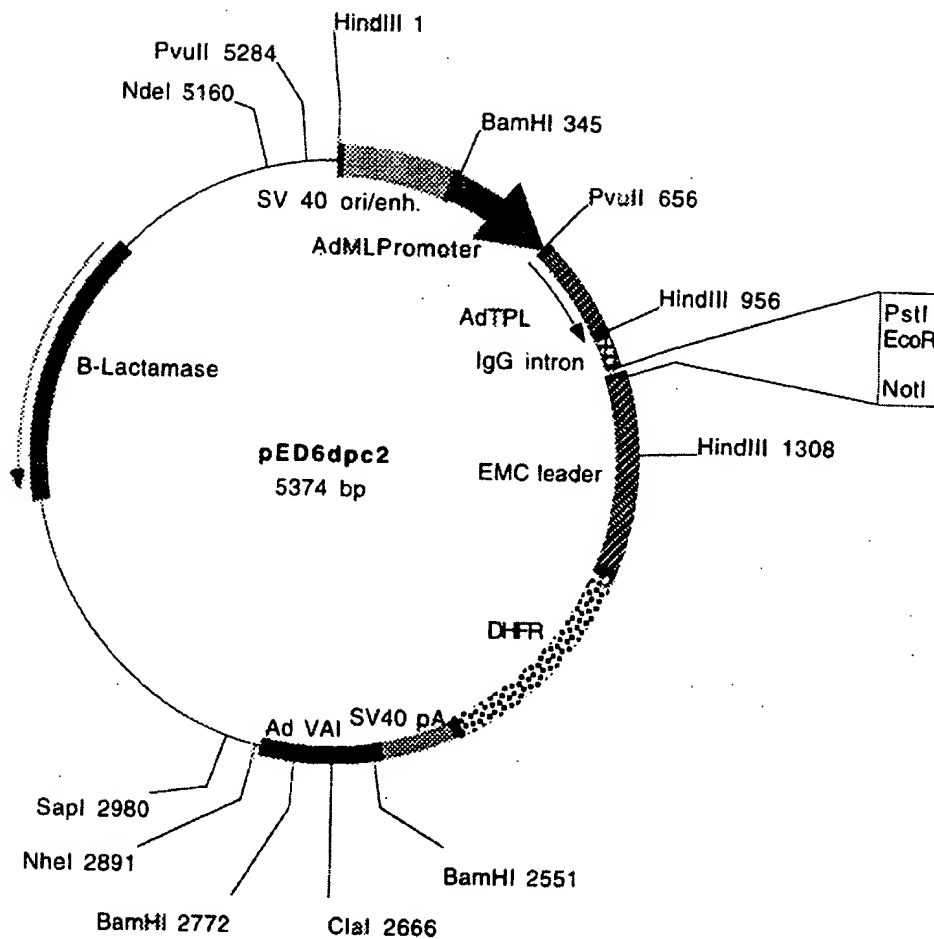
(a) the amino acid sequence of SEQ ID NO:118;

(b) a fragment of the amino acid sequence of SEQ ID NO:118, the fragment comprising eight contiguous amino acids of SEQ ID NO:118; and

(c) the amino acid sequence encoded by the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins.

FIGURE 1A

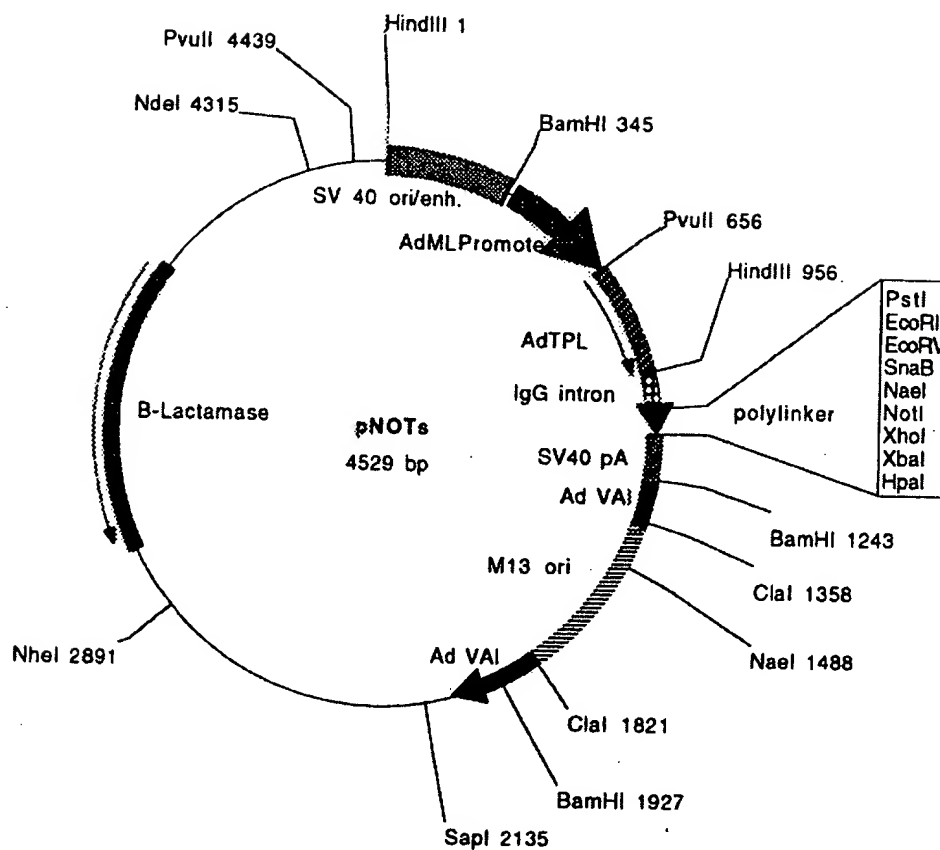


**Plasmid name:** pED6dpc2

**Plasmid size:** 5374 bp

**Comments/References:** pED6dpc2 is derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kaufman et al.(1991), NAR 19: 4485-4490.

FIGURE 1B



Plasmid name: pNOTs

Plasmid size: 4529 bp

**Comments/References:** pNOTs is a derivative of pMT2 (Kaufman et al, 1989. Mol. Cell. Biol. 9:1741-1750). DHFR was deleted and a new polylinker was inserted between EcoRI and HpaI. M13 origin of replication was inserted in the Clal site. SST cDNAs are cloned between EcoRI and NotI

## SEQUENCE LISTING

<110> Jacobs, Kenneth  
 McCoy, John M.  
 LaVallie, Edward R.  
 Collins-Racie, Lisa A.  
 Evans, Cheryl  
 Merberg, David  
 Treacy, Maurice  
 Agostino, Michael J.  
 Steininger II, Robert J.  
 Bowman, Michael R.  
 DiBlasio-Smith, Elizabeth  
 Widom, Angela  
 Genetics Institute, Inc.

<120> SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

<130> GI 6069-74A

<140>

<141>

<160> 180

<170> PatentIn Ver. 2.0

<210> 1

<211> 571

<212> DNA

<213> Homo sapiens

<400> 1

```

ttcttcgccca ggctctctgc tgactcaagt tcttcagttc acgatcttct agttgcagcg 60
atgagtgcac gagtgagatc aagatccaga ggaagaggag atggtcagga ggctcccgat 120
gtggttgcat tcgtggctcc cgggtgaatct cagcaagagg aaccaccaac tgacaatcag 180
gatattgaac ctggacaaga gagagaagga acacctccga tcgaagaacg taaagtagaa 240
ggtgattgcc aggaaatgga tctggaaaag actcggagtg agcgtggaga tggctctgat 300
gtaaaagaga agactccacc taatcctaag catgctaaga ctaaagaagc aggagatggg 360
cagccataag ttaaaaagaa gacaagctga agctacacac atggctgatg tcacattgaa 420
aatgtgactg aaaatttgaa aattctctca ataaagtttg agttttctct gaaaaaaaaa 480
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 540
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a                    571

```

<210> 2

<211> 102

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Ser Ala Arg Val Arg Ser Arg Ser Arg Gly Arg Gly Asp Gly Gln
  1                      5                      10                      15

Glu Ala Pro Asp Val Val Ala Phe Val Ala Pro Gly Glu Ser Gln Gln
          20                      25                      30

Glu Glu Pro Pro Thr Asp Asn Gln Asp Ile Glu Pro Gly Gln Glu Arg
          35                      40                      45

Glu Gly Thr Pro Pro Ile Glu Glu Arg Lys Val Glu Gly Asp Cys Gln

```

50

55

60

Glu Met Asp Leu Glu Lys Thr Arg Ser Glu Arg Gly Asp Gly Ser Asp  
 65 70 75 80

Val Lys Glu Lys Thr Pro Pro Asn Pro Lys His Ala Lys Thr Lys Glu  
 85 90 95

Ala Gly Asp Gly Gln Pro  
 100

&lt;210&gt; 3

&lt;211&gt; 2709

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

gaggaaacct ctcgctgggg ctaggagttc ggcgggggcg gcgcccggcg ctgcccagct 60  
 ggcaggtgcg aagcgtctgc acctggcggg cgatggcgcc cgatggcgcc gccccgggat 120  
 agcgtggggc agcgtgcggg gccccggcg gcacgcccgc acctctcccc agccctggcg 180  
 tgggcccagc ccggcccagg cagcaatggg gttcctgcag ctgctgggtc tagcgggtct 240  
 ggcacccgaa caccgggtgg ctgggtgcagc cgaggtcttc gggaattcca gcgaggggtct 300  
 tattgaattt tctgtgggga aatttagata cttcgagctc aataggccct ttccagagga 360  
 agctattttg catgatattt caagcaatgt gacttttctt attttccaaa tacactcaca 420  
 gtatcagaat acaactgttt ccttttctcc gactctcctt tccaattcct cggaacagg 480  
 cactgccagt ggactggttt tcatccttag accagagcag agtacatgca cttggtactt 540  
 ggggacttca ggcatacagc ctgtccagaa tatggctatc ctactctcct actcagaaaag 600  
 agatcctgtc cctggaggct gtaatttga gttcgattta gatattgat ccaacattta 660  
 cttggagtat aatttctttg aaacgactat caagtttgcc ccagcaaacc taggctatgc 720  
 gagaggcgta gatccccac catgtgacgc tgggacagac caggactcca ggtggagggt 780  
 gcagtatgat gtctatcagt attttctgcc tgagaatgac ctactgagg agatgttgc 840  
 gaagcatctg cagaggatgg tcagtgtgcc ccagggtgaag gccagtgtc tcaagggtgt 900  
 taccctaaca gctaatagata agacaagtgt ttcttctcct tccctcccgg gacaagggtg 960  
 catatacaat gtcatgtttt gggacccgtt tctaaataca tctgtgcctt acattcctgc 1020  
 tcacacatac gcttgagctt ttgaggcagg agagggtagt tgtgcttccc taggaagagt 1080  
 gtcttccaaa gtgttcttca ctctttttgc cctgcttggg ttcttcattt gtttcttttg 1140  
 acacagattc tggaaaacag aattattctt cataggcttt atcatcatgg gattcttctt 1200  
 ttataactg attacaagac tgacacctat caagtatgat gtgaatctga ttctgacagc 1260  
 tgtactgga agcgtcggtg gaatgttctt ggtagctgtg tgggaggcat ttggaactct 1320  
 ctgactctgc atgctctgtg ttggactagt gctgggggtc ctcatctcgt cagtactttt 1380  
 ctttactcca ctgggaaacc taaagatttt tcatgatgat ggtgtattct gggtcacttt 1440  
 ctcttgcata gctatcctca ttccagtagt ttcatgggc tgcctaagaa tactgaacat 1500  
 actgacttgt ggagtcattg gctcctatc ggtgggttta gccattgaca gttactgggtc 1560  
 cacaagcctt tctacatca ctttgaacgt actcaagaga gcgctcaaca aggatttcca 1620  
 cagagctttc acaaatgtgc cttttcaaac taatgacttc attatcctgg cagtatgggg 1680  
 catgctggct gtaagtggaa ttacgttaca gattogaaga gagagaggac gaccgttctt 1740  
 cctccccac ccatacaagt tatgggaagca agagagagag cgccgagtga caaacattct 1800  
 ggaccctagc taccacattc ctccattgag agagaggctc tatggccgat taaccagat 1860  
 taaagggctc ttccagaagg agcagccagc tggagagaga acgcctttgc ttctgtagat 1920  
 gccagggggc ttggtcagtg tgctcagct ttggagttca tgcttgaggt ggttcaacag 1980  
 tctctgggtc aagtctaata agagatcagg catatatatc tgttctttgc ataataattat 2040  
 ggtgccctta ttgatatatg gtaaggggtg actaggggat taggatgatt gtaagagaat 2100  
 gagaaagatg accaaaagggt tgggtgtagg gagggctttt cttatttcca aatacttgag 2160  
 aaattacctt ttggtttaca aatctatgat caacttatc cattaaatag atacattaaa 2220  
 aaaattaaaa actgattctt ctgcagagca ctggtgtttc tttttataac cccttgaaac 2280  
 aagtctctca cstgagcctg tctaaacttt cggagggagt ttattattga gtctttatct 2340  
 gtgacagtat ttggagattt agggatttga tacttaggcc tttgaatttt agaatacaaa 2400  
 aagagaagca agccagacat ggtggctcac acctgtaac ccaatactgg gaggccaagg 2460  
 tgggagtatc gcttgagccc aggagtttga gaccgacatg ggcaacatga caagacccca 2520

tctctgcaaa aagattaaaa agttggccag gcatgggtggc acatgcctgc tcccagctcc 2580  
 cggggagact gagatggggg gatccctgg agccctgaag attgaggctg cagtgagcct 2640  
 tgattgtgtc actgcactcc agcttgggtg acagagaccc tgtctcgaga aattaaaaaa 2700  
 aaaaaaaaaa 2709

<210> 4

<211> 570

<212> PRT

<213> Homo sapiens

<400> 4

Met Gly Phe Leu Gln Leu Leu Val Val Ala Val Leu Ala Ser Glu His  
 1 5 10 15

Arg Val Ala Gly Ala Ala Glu Val Phe Gly Asn Ser Ser Glu Gly Leu  
 20 25 30

Ile Glu Phe Ser Val Gly Lys Phe Arg Tyr Phe Glu Leu Asn Arg Pro  
 35 40 45

Phe Pro Glu Glu Ala Ile Leu His Asp Ile Ser Ser Asn Val Thr Phe  
 50 55 60

Leu Ile Phe Gln Ile His Ser Gln Tyr Gln Asn Thr Thr Val Ser Phe  
 65 70 75 80

Ser Pro Thr Leu Leu Ser Asn Ser Ser Glu Thr Gly Thr Ala Ser Gly  
 85 90 95

Leu Val Phe Ile Leu Arg Pro Glu Gln Ser Thr Cys Thr Trp Tyr Leu  
 100 105 110

Gly Thr Ser Gly Ile Gln Pro Val Gln Asn Met Ala Ile Leu Leu Ser  
 115 120 125

Tyr Ser Glu Arg Asp Pro Val Pro Gly Gly Cys Asn Leu Glu Phe Asp  
 130 135 140

Leu Asp Ile Asp Pro Asn Ile Tyr Leu Glu Tyr Asn Phe Phe Glu Thr  
 145 150 155 160

Thr Ile Lys Phe Ala Pro Ala Asn Leu Gly Tyr Ala Arg Gly Val Asp  
 165 170 175

Pro Pro Pro Cys Asp Ala Gly Thr Asp Gln Asp Ser Arg Trp Arg Leu  
 180 185 190

Gln Tyr Asp Val Tyr Gln Tyr Phe Leu Pro Glu Asn Asp Leu Thr Glu  
 195 200 205

Glu Met Leu Leu Lys His Leu Gln Arg Met Val Ser Val Pro Gln Val  
 210 215 220

Lys Ala Ser Ala Leu Lys Val Val Thr Leu Thr Ala Asn Asp Lys Thr  
 225 230 235 240

Ser Val Ser Phe Ser Ser Leu Pro Gly Gln Gly Val Ile Tyr Asn Val  
 245 250 255

Ile Val Trp Asp Pro Phe Leu Asn Thr Ser Ala Ala Tyr Ile Pro Ala



260	265	270
His Thr Tyr Ala Cys Ser Phe Glu Ala Gly Glu Gly Ser Cys Ala Ser 275 280 285		
Leu Gly Arg Val Ser Ser Lys Val Phe Phe Thr Leu Phe Ala Leu Leu 290 295 300		
Gly Phe Phe Ile Cys Phe Phe Gly His Arg Phe Trp Lys Thr Glu Leu 305 310 315 320		
Phe Phe Ile Gly Phe Ile Ile Met Gly Phe Phe Phe Tyr Ile Leu Ile 325 330 335		
Thr Arg Leu Thr Pro Ile Lys Tyr Asp Val Asn Leu Ile Leu Thr Ala 340 345 350		
Val Thr Gly Ser Val Gly Gly Met Phe Leu Val Ala Val Trp Trp Arg 355 360 365		
Phe Gly Ile Leu Ser Ile Cys Met Leu Cys Val Gly Leu Val Leu Gly 370 375 380		
Phe Leu Ile Ser Ser Val Thr Phe Phe Thr Pro Leu Gly Asn Leu Lys 385 390 395 400		
Ile Phe His Asp Asp Gly Val Phe Trp Val Thr Phe Ser Cys Ile Ala 405 410 415		
Ile Leu Ile Pro Val Val Phe Met Gly Cys Leu Arg Ile Leu Asn Ile 420 425 430		
Leu Thr Cys Gly Val Ile Gly Ser Tyr Ser Val Val Leu Ala Ile Asp 435 440 445		
Ser Tyr Trp Ser Thr Ser Leu Ser Tyr Ile Thr Leu Asn Val Leu Lys 450 455 460		
Arg Ala Leu Asn Lys Asp Phe His Arg Ala Phe Thr Asn Val Pro Phe 465 470 475 480		
Gln Thr Asn Asp Phe Ile Ile Leu Ala Val Trp Gly Met Leu Ala Val 485 490 495		
Ser Gly Ile Thr Leu Gln Ile Arg Arg Glu Arg Gly Arg Pro Phe Phe 500 505 510		
Pro Pro His Pro Tyr Lys Leu Trp Lys Gln Glu Arg Glu Arg Arg Val 515 520 525		
Thr Asn Ile Leu Asp Pro Ser Tyr His Ile Pro Pro Leu Arg Glu Arg 530 535 540		
Leu Tyr Gly Arg Leu Thr Gln Ile Lys Gly Leu Phe Gln Lys Glu Gln 545 550 555 560		
Pro Ala Gly Glu Arg Thr Pro Leu Leu Leu 565 570		

<210> 5  
<211> 3063  
<212> DNA  
<213> Homo sapiens

<400> 5

```
cgaggcgcgg gtggtgccgg tggcggcggc gggggagcgc gggacaggag gcttcgggga 60
agatggaccc ggcccccctcg ctgggctgca gcctcaagga tgtgaagtgg agctcgggtg 120
ccgtgccgct cgacctcctg gtcagcactt accggctgcc ccagatcgcg cgcttgga 180
acggagagtg cgtagaaggg ctgcgggaaa atgactatct gctgattcat tcctgccg 240
agtggaccac catcactgcc cacagcttgg aggaggttca ctatgtcatt gggccaaaga 300
tagagattcc ggtacattat gcagggcaat tcaagctgct ggaacaagac cgagatataa 360
aggagccagt gcaatatttc aacagtgtgg aggaggtggc taaggcattt cctgaacg 420
tgtacgtcat ggaggatata acattcaacg tgaagggtgc ttcaggtgaa tgcaatga 480
acactgaagt ttacaacatc accctgtgta ctggggatga actcactcta atgggggcag 540
gcagaaatcc ttcatgcaaa gacattcaag gaaaagtcac gactcaacac aatcttcaa 600
aagattggga agctcaattc catcagcaag ctgggaaaag gcaaaatgcc gtgcctcatt 660
tgtatggaac accggacca cgaagcatt agccttccat tccagtgcga gggcagatt 720
agcaccccgga agtcccctgg aacttcagat gcaaaagggc gaacacacca tccgccacat 780
tgtggagaaa accaggcttc ctgtgaatgt gactgtgcca agccctccac cgagaaccc 840
atacgacctc cacttcatcc gtgaggggca ccgctataag tttgtgaaca tccagacca 900
gacgggtggg gtttctgtgt tgctgcggga caacaagatc ctcccatgc acttctctt 960
gcacttgact gtcccagat tcagcctccc agaacacctg gtgaaggagg agagctggcc 1020
cgaaacctgt gtccatcact ggctagggtat ctgccaagaa cagttcgaca tcgatgagta 1080
ttcacgggct gtccgtgatg tgaaaccga ctggaatgaa gaatgcaaga gccccaagaa 1140
gggtcgggtc tctggccaca accacgtgcc caattcgctc agctacgccc gcgatgagct 1200
caccagctcc ttcaccgac tctcggctctg tgtgtatggc aacaatctcc atggcaacag 1260
tgaggtgaac cttcatggtt gcaggaccc ggggggagat tgggtccctt ttcctcatga 1320
catcctgccc tatcaggact ctggagatag tgggagcgac taccttttcc cagaagctag 1380
tgaagaatca gcaggcatcc cgggaaagtc agaacttccc tacgaagagc tgtggctgga 1440
ggaaggcaag ccagccatc agcctctcac tcgctctctg agcgagaaga acagatgtga 1500
tcagtttaga ggttctgtcc gatccaaatg tgcgacttct cctcttccca tccctgggac 1560
tctgggagca gcagtgaagt cttcagatac tgccctacct ccacctccag tgcctcccaa 1620
atctgaagcc gtcagagaag aatgccggct cctgaacgcc ccacctgttc caccgcgaag 1680
cgcaaagcct ttgtccacca gtccctccat ccctcctcgc acagtcaagc cagcgcgga 1740
acagactcgc tctcccagcc ccacctgtc ctactattct tcagggtac acaacatcgt 1800
cactaaaact gacacaaatc cttctgaaag cactctgtt tctgtctatc catgtaaccg 1860
agtgaaaact gattctgtgg acctgaaatc cccgtttgga agtccttctg ctgaagctgt 1920
gtcctctcgg ctctcatggc ctaaccatta ttcaggagca tcagaaagcc agaccaggag 1980
tgacttctct ctggatccaa gcaggagtta tagttacct agacaaaaga cgccaggcac 2040
accaaagaga aactgcccag caccttttga ttttgatggc tgtgagctcc tggccagccc 2100
cactagccca gtcactgcag aattcagtag cagcgtctct ggtgtgacca agtcagccag 2160
ctactctctg gagagcacag atgtgaaatc tcttgcaagt ggtgtgacaa agcagagtag 2220
gtcatgccct gccttaccct ccagggtccc aaaactagtg gaagagaagg tgcctccga 2280
aacatctcct ttgcctctga aaattgatgg tgctgaggaa gaccccaagt ctgggtcacc 2340
agatctctcg gaggaccagt attttgtaa aaaggcatg caggacatct tctctgctc 2400
ctaccctttc tcatctccgc tccatctcca gctggcccc agatcctgtg gcgacgggtc 2460
cccatggcag ccacctgctg acctatcagg actctctata gaggaagtgt ccaagtcact 2520
acgggttcatt ggtttgtccg aagatgtcat atcattcttt gttactgaaa agattgatgg 2580
gaacctgctt gttcagctaa cggaagaaat cctctcagag gatttcaa attgagcaaatt 2640
gcagggtgaag aagataatgc aattcattaa tggctggagg cccaaaatat agccaaataa 2700
ccccgggcca gcatggaaca aaactgatca atgcgtgtgc tagaaggggt gggctgggac 2760
acaatttcat gtttttgac taaaaacctt ctctgtaaat agggataaga gaaactctta 2820
ctatgcagat tacgtttttg aatgggtgac aggcatttt gtacatcaat aaaaatgctg 2880
tacagaacac ttggaggtgt gcctgtacg tcaactcaaca aacactcagc agctgctaaa 2940
agaaaaaag gcatgtgcag agaaatcatt cttaccaag taggtttatg tgagaaggta 3000
tgatatattat tacaaaatag ccaaagctga aagacataaa aatctttaa aaaaaaaa 3060
aaa 3063
```

<210> 6

<211> 647  
 <212> PRT  
 <213> Homo sapiens

<400> 6

```

Met Gln Lys Gly Glu His Thr Ile Arg His Ile Val Glu Lys Thr Arg
  1              5              10              15

Leu Pro Val Asn Val Thr Val Pro Ser Pro Pro Pro Arg Asn Pro Tyr
      20              25              30

Asp Leu His Phe Ile Arg Glu Gly His Arg Tyr Lys Phe Val Asn Ile
      35              40              45

Gln Thr Lys Thr Val Val Val Cys Cys Val Leu Arg Asp Asn Lys Ile
      50              55              60

Leu Pro Met His Phe Pro Leu His Leu Thr Val Pro Lys Phe Ser Leu
      65              70              75              80

Pro Glu His Leu Val Lys Gly Glu Ser Trp Pro Glu Thr Leu Val His
      85              90              95

His Trp Leu Gly Ile Cys Gln Glu Gln Phe Asp Ile Asp Glu Tyr Ser
      100              105              110

Arg Ala Val Arg Asp Val Lys Thr Asp Trp Asn Glu Glu Cys Lys Ser
      115              120              125

Pro Lys Lys Gly Arg Cys Ser Gly His Asn His Val Pro Asn Ser Leu
      130              135              140

Ser Tyr Ala Arg Asp Glu Leu Thr Gln Ser Phe His Arg Leu Ser Val
      145              150              155              160

Cys Val Tyr Gly Asn Asn Leu His Gly Asn Ser Glu Val Asn Leu His
      165              170              175

Gly Cys Arg Asp Leu Gly Gly Asp Trp Ala Pro Phe Pro His Asp Ile
      180              185              190

Leu Pro Tyr Gln Asp Ser Gly Asp Ser Gly Ser Asp Tyr Leu Phe Pro
      195              200              205

Glu Ala Ser Glu Glu Ser Ala Gly Ile Pro Gly Lys Ser Glu Leu Pro
      210              215              220

Tyr Glu Glu Leu Trp Leu Glu Glu Gly Lys Pro Ser His Gln Pro Leu
      225              230              235              240

Thr Arg Ser Leu Ser Glu Lys Asn Arg Cys Asp Gln Phe Arg Gly Ser
      245              250              255

Val Arg Ser Lys Cys Ala Thr Ser Pro Leu Pro Ile Pro Gly Thr Leu
      260              265              270

Gly Ala Ala Val Lys Ser Ser Asp Thr Ala Leu Pro Pro Pro Pro Val
      275              280              285

Pro Pro Lys Ser Glu Ala Val Arg Glu Glu Cys Arg Leu Leu Asn Ala

```

290	295	300
Pro Pro Val Pro Pro Arg Ser Ala Lys Pro Leu Ser Thr Ser Pro Ser		
305	310	315 320
Ile Pro Pro Arg Thr Val Lys Pro Ala Arg Gln Gln Thr Arg Ser Pro		
	325 330	335
Ser Pro Thr Leu Ser Tyr Tyr Ser Ser Gly Leu His Asn Ile Val Thr		
	340 345	350
Lys Thr Asp Thr Asn Pro Ser Glu Ser Thr Pro Val Ser Cys Tyr Pro		
	355 360	365
Cys Asn Arg Val Lys Thr Asp Ser Val Asp Leu Lys Ser Pro Phe Gly		
	370 375	380
Ser Pro Ser Ala Glu Ala Val Ser Ser Arg Leu Ser Trp Pro Asn His		
	385 390	395 400
Tyr Ser Gly Ala Ser Glu Ser Gln Thr Arg Ser Asp Phe Leu Leu Asp		
	405 410	415
Pro Ser Arg Ser Tyr Ser Tyr Pro Arg Gln Lys Thr Pro Gly Thr Pro		
	420 425	430
Lys Arg Asn Cys Pro Ala Pro Phe Asp Phe Asp Gly Cys Glu Leu Leu		
	435 440	445
Ala Ser Pro Thr Ser Pro Val Thr Ala Glu Phe Ser Ser Ser Val Ser		
	450 455	460
Gly Cys Pro Lys Ser Ala Ser Tyr Ser Leu Glu Ser Thr Asp Val Lys		
	465 470	475 480
Ser Leu Ala Ala Gly Val Thr Lys Gln Ser Thr Ser Cys Pro Ala Leu		
	485 490	495
Pro Pro Arg Ala Pro Lys Leu Val Glu Glu Lys Val Ala Ser Glu Thr		
	500 505	510
Ser Pro Leu Pro Leu Lys Ile Asp Gly Ala Glu Glu Asp Pro Lys Ser		
	515 520	525
Gly Ser Pro Asp Leu Ser Glu Asp Gln Tyr Phe Val Lys Lys Gly Met		
	530 535	540
Gln Asp Ile Phe Ser Ala Ser Tyr Pro Phe Ser Ser Pro Leu His Leu		
	545 550	555 560
Gln Leu Ala Pro Arg Ser Cys Gly Asp Gly Ser Pro Trp Gln Pro Pro		
	565 570	575
Ala Asp Leu Ser Gly Leu Ser Ile Glu Glu Val Ser Lys Ser Leu Arg		
	580 585	590
Phe Ile Gly Leu Ser Glu Asp Val Ile Ser Phe Phe Val Thr Glu Lys		
	595 600	605
Ile Asp Gly Asn Leu Leu Val Gln Leu Thr Glu Glu Ile Leu Ser Glu		

610

615

620

Asp Phe Lys Leu Ser Lys Leu Gln Val Lys Lys Ile Met Gln Phe Ile  
 625 630 635 640

Asn Gly Trp Arg Pro Lys Ile  
 645

&lt;210&gt; 7

&lt;211&gt; 892

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 7

```

ggcagagct cgtgcactca tggcgacccg gaacccccct cccaagact atgaaagtga 60
tgacgactct tatgaagtgt tggatttaac tgagtatgcc agaagacacc agtgggtggaa 120
tcgagtgttt ggccacagtt cgggacctat ggtagaaaaa tactcagtag ctaccagat 180
tgtaattgggt gccgttactg gctgggtgtgc aggatttctg ttccagaaaag ttggaaaact 240
tgcagcaact gcagtaggtg gtggctttct tcttcttcag attgctagtc atagtggcta 300
tgtgcagatt gactggaaga gagttgaaaa agatgtaaat aaagcaaaaa gacagattaa 360
gaaacgagcg aacaaagcag cacctgaaat caacaattta attgaagaag caacagaatt 420
tatcaagcag aacattgtga tatccagtgg atttgtggga ggctttttgc tcggacttgc 480
atcttaagga catgaatatt ctcccataac ggattcaact atgagaagag aagtggcagc 540
aataaggcag tctctcaaaa gtcatactgc cagagtctct agggcaagga gaaacaacta 600
gctggacaat actcaattca caacttagca ttttgccatc tgaagcttgg caaactagta 660
tctgctgtaa aacaacctat atggtagtg aaccgtagta ttcctgagca aaacgtggct 720
ttcatcgctt tgtaaaaatt tgcattctgt tagaaactag cctataaaat atcaccattg 780
gatgtagata tggagagaaa agaaatatgt tgggtttatt gcttagcgaa atattctctt 840
tttatttaaa taaaatgttc ttcattgtgt tttaaaaaaa aaaaaaaaaa aa 892

```

&lt;210&gt; 8

&lt;211&gt; 155

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

```

Met Ala Thr Arg Asn Pro Pro Pro Gln Asp Tyr Glu Ser Asp Asp Asp
  1           5           10           15

Ser Tyr Glu Val Leu Asp Leu Thr Glu Tyr Ala Arg Arg His Gln Trp
          20           25           30

Trp Asn Arg Val Phe Gly His Ser Ser Gly Pro Met Val Glu Lys Tyr
          35           40           45

Ser Val Ala Thr Gln Ile Val Met Gly Gly Val Thr Gly Trp Cys Ala
          50           55           60

Gly Phe Leu Phe Gln Lys Val Gly Lys Leu Ala Ala Thr Ala Val Gly
          65           70           75           80

Gly Gly Phe Leu Leu Leu Gln Ile Ala Ser His Ser Gly Tyr Val Gln
          85           90           95

Ile Asp Trp Lys Arg Val Glu Lys Asp Val Asn Lys Ala Lys Arg Gln
          100          105          110

Ile Lys Lys Arg Ala Asn Lys Ala Ala Pro Glu Ile Asn Asn Leu Ile
          115          120          125

```

Glu Glu Ala Thr Glu Phe Ile Lys Gln Asn Ile Val Ile Ser Ser Gly  
 130 135 140

Phe Val Gly Gly Phe Leu Leu Gly Leu Ala Ser  
 145 150 155

<210> 9  
 <211> 1850  
 <212> DNA  
 <213> Homo sapiens

<400> 9  
 cactcctact gcggtgcta tgaagcttac tggttgtgat gtgttataat ttagtctgtt 60  
 tttttgattg aatgcagttt aatgtttcca gaaagccaaa gtaattttct tttcagatat 120  
 gcaaggcttt ggtgggtcca aaaaatgtct atcacaagcc attttttcct tttcctctct 180  
 cgaaaagtta aaatatctat gtgttatctc caaacctctc tacctatgta tctgcctgtc 240  
 tgtccatcat ctcccttcct ccctatctct gtgtatctgg atggcagccg ctgcccargg 300  
 gagtggctgt ggggaggcca ggtactgtct ttgcctgtgg gtccagctga gccatccctg 360  
 ctgggtgatg ctgggcaaga cccttgcccc gtctgggcct tggtctctc accctcgcca 420  
 tgagcgggaa gatgactctc agttccttcc acctcttaga catgggtgagg taacagacat 480  
 caaaagcttt tctgaaatct tcagaagaaa tagttccatt acagaaaact cttcaaaata 540  
 aatagtagtg aaaactttta aaaactctca ttggagtaag tcttttcaag atgatcctcc 600  
 acaatggagg cagcgttcct acttgtcatc acacagctga agacattgtt tcttaggtgt 660  
 gaaatcgggg acaaaggaca aacagagaca cagggcattg ttcattggag gcacgtctac 720  
 cctcctgggt gttctgtggg aatttcctgt gtgaggaaaa cgtggccaca ggggttgtgt 780  
 gtacccaccc tccccggcg agatggccct cgccctgtgc cgtgcttcc accctcgcca 840  
 ctccatggca gcttttggtc tgtttccggc tctgccctct gccctgaact ctcacccggc 900  
 ttgtacctgc ctgctggacc cctccacctg gaggccagcc catgtctcag gccagccct 960  
 agcctcttct cctcaaattc taagtgtttt ctcttttagt ttccttggtt ttgtgaatgg 1020  
 atcatgtgtc tctaggtata aacctgacat catctctcca cccggttac ctccaccaga 1080  
 tctccccagt tctgtctcca tcttctacct gcagctgtc tgttctcatg gtcactgtgt 1140  
 catcactgag tctggaccct tgttatcatt ttcaaactgg cctccttccc tctgtcccca 1200  
 cttcttaaag tcacctgtcc attgccacca gattaagctt tctccagcca gatcacctct 1260  
 cttctgagaaa cctccattga catggaaaca ccattgtctg gcacacatac tcacatactc 1320  
 accttcccg tttgatcccc acacatcttt ccagcctccc ctccactcc actcctgtct 1380  
 cctcctcca cctccccatc ctcttgtctc cctccccctc tgaatccagc ccagcggggc 1440  
 ttctcctgcc tccatcacat cacagaagta cctcctgctt ctgggtttta ttagagcctt 1500  
 ccccgattac attttctct gaatttttct ctatctacat ttgatctgtc atgttttaac 1560  
 cccctacttc taagggaact tctctaactc cttatctctc tccccaaata gtgttttctt 1620  
 cctctgggtt cttataatgt tggatatcaat ctacagcat ttagtgcttc ctgctgggtg 1680  
 tgacagttac ctgtgtgcat gtgcaatttc taatttcca cgctagactg tgagcttctc 1740  
 aaggcaagaa tcatgccttg ttggtttctg tattctcat ggtgccaac acagtgcctt 1800  
 ctacattgca ggcgtgaat aaacattttt aaagcaaaaa aaaaaaaaaa 1850

<210> 10  
 <211> 206  
 <212> PRT  
 <213> Homo sapiens

<400> 10  
 Met Ala Leu Gly Leu Cys Arg Cys Phe His Pro Arg His Ser Met Ala  
 1 5 10 15  
 Ala Phe Gly Leu Phe Pro Ala Leu Pro Ser Ala Leu Asn Ser His Pro  
 20 25 30  
 Ala Cys Thr Cys Leu Leu Asp Pro Ser Thr Trp Arg Pro Ala His Val  
 35 40 45

Ser Gly Pro Ala Leu Ala Ser Ser Pro Gln Ile Leu Ser Val Phe Ser  
 50 55 60  
 Leu Gly Phe Pro Gly Phe Val Asn Gly Ser Cys Val Ser Arg Tyr Lys  
 65 70 75 80  
 Pro Asp Ile Ile Ser Pro Pro Gly Leu Pro Pro Pro Asp Leu Pro Ser  
 85 90 95  
 Ser Val Ser Ile Phe Tyr Leu Gln Leu Leu Cys Ser His Gly His Cys  
 100 105 110  
 Cys Ile Thr Glu Ser Gly Pro Leu Leu Ser Phe Ser Asn Trp Pro Pro  
 115 120 125  
 Ser Leu Val Pro His Phe Leu Lys Ser Pro Val His Cys His Gln Ile  
 130 135 140  
 Lys Leu Ser Pro Ala Arg Ser Pro Leu Ser Glu Lys Pro Pro Leu Thr  
 145 150 155 160  
 Trp Lys His His Cys Leu Ala His Ile Leu Thr Tyr Ser Pro Ser Arg  
 165 170 175  
 Leu Asp Pro His Thr Ser Phe Gln Pro Pro Leu Pro Leu His Ser Leu  
 180 185 190  
 Leu Pro Pro Pro Pro Pro His Pro Leu Val Ser Pro Pro Leu  
 195 200 205

&lt;210&gt; 11

&lt;211&gt; 2216

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 11

cttgtaagtt actgtagtg aattgttttt tacgtttcat ttaataattg ctgctaaagg 60  
 tgatgtttac tgataaatca ttttaaaatt tttttgtttt gaaaagtaaa tttatcccc 120  
 atgatgttag atacatttaa attattaagt cttttcagag atgagatggg gacaggaagt 180  
 tattttgagc cttacaatat tatttagccc aataaaagat gcattgaagc tcttatatat 240  
 tatgagtttg aaaaattttg aaggtagcat attgaagtga tctataaata tcttcagtcc 300  
 tctctgaagt gtgggtattt cttctatcta aaaaatacat acagtgactg tcttcaaadc 360  
 tacttggttc ttgaccaaata argagctaata gggtaataga tacctttttg tttgtttgtt 420  
 tgtttggttg ttttttggtt ttttttttaa ggggtctcact cttttgccc ggtggtgagt 480  
 cagtggcaca atcacggctc ccaggctaata gtttttattt ttaatttgta attttttttt 540  
 tatttttttt gttgagatgg agttgctcca tggtgcacag gctgttctca aactcctaag 600  
 ctcaagccat ctgcctgcst tggcctccca aagtgtggg attgtagaca taagccacct 660  
 caccagcct atgaatatct ttctaataat gtaagaatga ggtaattgtt ccatcagtct 720  
 aatacagata tattttcttc ctccaaaaca gtttattttg attgtttatt ttattttgat 780  
 tgtaactccg tcataactyg acatggaaaa tgctatatac tatgaaaact tagctgaaag 840  
 ggaagaattg ttttagaaag acaatattta aaacaccgca ctgccaatat attgatcctt 900  
 tatagttatt tcctaaaatg ctgttttcga aacattcctt ttccaccctg ttgtgtggct 960  
 tagaccatc tcgtaaatcg ttaattggaa agaggctaca gacaccagca gtgtgcgttc 1020  
 tgcaggtaca cgctgccaaa gtaattcctg ctcattccatg cctgtctct gtctctttta 1080  
 gagtcatacc ttatttgagt ataggtggct taattttgct agacttctg aaacactaa 1140  
 ggtggagtat cagaagtgat ttttagtcaca gttctgctgg agagcttaga ataacatcct 1200  
 cctttgggag gtggtcttg gtgcgtggat cttggtatag agtctttatt gtaagtctga 1260  
 taaaaaatgc taataaattt aatgtttttc ttccttaatt tattggcata gttcttcagg 1320

```

tagcacctca tttttattaa tgatattggg attaactatg aacaagctat atgtagacat 1380
ttgcatttaa ggacattgca gtgtttcaaa gatcccatca ttgcagcttg tatccttttag 1440
atccaatcgg aaactttctgg agtcttacat taatgctcat ttgagctaata tagtaatctg 1500
tttaaacaga ttgggaata ctttaaagat actgtagact atttatgtat agatagatca 1560
tattacccat taaaagtctg ggggaaaaaa ttttttaatt ttactcttct tatgtactga 1620
aaactttttt taaaaaagggt gatgatgaag ttcatctgt agcagcagcg cagctatgct 1680
ttaaaccaca caaaaggctg tgtccagggt cagcctcctt cacccttcst gccacgggtg 1740
aggattgaat aaccaggact tggggatatk gtttgtgtgc agggttattc tgtgtggtaa 1800
ggaatatttg ttccacattt atacattttc tttttccact cagctaagtt tctatcttga 1860
gagcatagtc caaagtgcaa aacttggtgt ttacaaggaa aattgtcttc cagaactcca 1920
ctgtcatcac ttccacaaa gtggaagttt gcatgaatat gctcagaatc taatattcaa 1980
tgttctgtta cattgtaagt gaagtccagc tacaaaatag atttaatata ttgaatttat 2040
ttgtacatat gcagagtacg gtatttctgt atggaatctg ctttattcct atttttccca 2100
actctgatga gtagaatatt aaatgtgttg ttatggaaat acagattatt gcttctatag 2160
gaagataatt atgaaaataa aacctgaaac tatataaata taataaaaaa aaaaaa 2216

```

&lt;210&gt; 12

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 12

```

Met Leu Phe Ser Lys His Ser Phe Phe Thr Leu Leu Cys Gly Leu Asp
  1             5             10             15

Pro Ser Arg Asn Leu Leu Ile Gly Lys Arg Leu Gln Thr Pro Ala Val
      20             25             30

Cys Val Leu Gln Val His Ala Ala Lys Val Ile Pro Ala His Pro Cys
      35             40             45

Pro Val Ser Val Ser Phe Arg Val Ile Pro Tyr Leu Ser Ile Gly Gly
      50             55             60

Leu Ile Leu Leu Asp Phe Leu Lys Thr Leu Arg Trp Ser Ile Arg Ser
      65             70             75             80

Asp Phe Ser His Ser Ser Ala Gly Glu Leu Arg Ile Thr Ser Ser Phe
      85             90             95

Gly Arg Trp Ser Trp Val Arg Gly Ser Trp Tyr Thr Val Phe Ile Val
      100             105             110

Ser Leu Ile Gln Asn Ala Asn Lys Phe Asn Val Phe Leu Pro
      115             120             125

```

&lt;210&gt; 13

&lt;211&gt; 1426

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 13

```

ctgggtctcc agggggagag cctggccctg tcctttgcta cccagggctg cccccaggcc 60
catgaagcca ataggagagc gtgtggcact ggcccacaaa ctgtccctgt cctgtcttcc 120
tcccagagcca tggcctctgc tagctccacc ttgaaggagc ccccacatc ctcccacac 180
tcccagagat gccaccactt gtgtctccac aatgtgtctc tgcccaccg ggttccgcac 240
tgtccgaccc ctgcacacca ctcatgtcac caggcggtgc atcatgttca tcccacatca 300
tttatttaag ctttctttg cttgtagggc attttgtatg tagagcagtt gaaaacagaa 360
cctcagaact taacatctgt cctgatgtta aagtgtttt catgaccacc ctgttatcta 420

```



```

tgatatatgta aagttaagga tgagatctta agtttacaat taaaaactca gtactcaata 480
tttaatatctt tactcgagct ttatggaagc caaatcatgc atgtgtgtgt gtgcgtgtgt 540
gcaagctttg aacctccttc cacagccgca tcttctcatg acacaaagct tttgataagt 600
actttcctgt gggtcgctca gggcctcata gcatctcatt caattacaag aatagaggcc 660
agacacgggtg gcgcatgcct gtagtcccag ctaactggga ggctgaggca ggaggatcac 720
ttgagcccag gagattgagg ctgcagttag catgatcgcg aactgact ccagcctggg 780
tgacgggtgag actttgtctc aaaaaaaaaa aaaaaaaca tggaaggcag acagcaagtc 840
cctgaggaca catcacacag tgtcctgtag ctaagtgtct agggaaaaaac aaaaactcca 900
aacccctcag tggatgagga caaggtcgca gaaaggcatt ctgttgacag atgaacagcc 960
gaaagctggc cagaccctcc tgtatgcctc tgcccttgtc ctgtgggttg agggggtctg 1020
accaggaggc cacctacagc aggaagttag gctgccatgt ttccttgaga cacagtgcc 1080
tctccccagc tctgtccctg tagtcacctg ccggtgggcg aggatcctct ccctgggata 1140
agcactccca gcccggttta tcagaaacac aggcaaggaa attggaactg ccaccagcc 1200
cagcatgggtg gctcaattgg ttggttgctg tgcagttgt ctcttcgttt tgtaaggtt 1260
tttaataagt acgtttggca taatgtcttt taatgggttt gtaatatattg taacggtttt 1320
agcagcctat aacttttcag ctgggtgcttt tacttaggga aaaaaacaat ttgtaaatac 1380
agaacattgt ttaaaagaca taaccataga aaaaaaaaaa aaaaaa 1426

```

&lt;210&gt; 14

&lt;211&gt; 80

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

```

Met Pro Pro Leu Val Ser Pro Gln Cys Ala Pro Ala His Pro Gly Ser
  1              5              10              15

```

```

Ala Leu Ser Asp Pro Cys Thr Pro Leu Met Ser Pro Arg Arg Ala Ser
      20              25              30

```

```

Cys Ser Ser Pro Ser Ile Tyr Leu Ser Leu Ser Leu Leu Val Gly His
  35              40              45

```

```

Phe Val Cys Arg Ala Val Glu Asn Arg Thr Ser Glu Leu Asn Ile Cys
  50              55              60

```

```

Pro Asp Val Lys Val Leu Phe Met Thr Thr Leu Leu Ser Met Tyr Met
  65              70              75              80

```

&lt;210&gt; 15

&lt;211&gt; 2364

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 15

```

gaagcgggctg ctgtaggcgc cgacggagcg agcgggctg cgagcggggc gacagtggcg 60
tgggatctgc ctctctgcga gcagctggga gcggcggcgg cggcgccatg agcgggggca 120
ccccttacat cggcagcaag atcagcctca tctccaaggc ggagatccgc tacgagggca 180
tcctctacac catcgacacc gaaaactcca ccgtagccct tgccaaagtt cgatcctttg 240
gtacagaaga cagaccgaca gatcgctcaa taccacctcg agatgaagtc tttgaataca 300
ttatattccg tgggagtgc attaaagacc ttactgtttg tgagccacca aaaccacagt 360
gtctcttgcc tcaagacca gctattgttc agtctcact aggtcctcag acttcttcat 420
tccagtcctat gggttcttat ggaccttctg gcaggatgcc cacatacagt cagttcagtc 480
cgagttcctt agttgggcag cagtttggtg ctggttggtg tgctggaagc tctttgacat 540
cctttggaac agaaacatca aacagtggta ccttacccca aagtagtgcg gttgggtctg 600
cctttacaca ggatacaaga tctctaaaaa cacagttatc tcaaggtcgc tcaagccctc 660
agtttagacc tttgagaaaa agcccaacca tggaacaagc agtgcagacc gcctcagccc 720
acttacctgc tccagcagct gttgggagaa ggagtctgt atcaaccagg cctttgccat 780
ctgccagcca aaaggcagga gagaatcagg agcacaggca agctgaagta cacaaagttt 840

```

```

caaggccaga aaatgagcaa ctcagaaatg ataacaagag acaagtagct ccagggtgctc 900
cttcagctcc aaggagaggg cgtgggggtc atcggggtgg caggggaaga tttggtattc 960
ggcgagatgg gccaatgaaa tttgagaaag actttgactt tgaaagtgc aatgcacaat 1020
tcaacaagga agagattgac agagagtttc ataataaact taaattaaaa gaagataaac 1080
ttgagaaaca ggagaagcct gtaaattggtg aagataaagg agactcagga gttgataccc 1140
aaaacagtga aggaaatgcc gatgaagaag atccacttgg acctaattgc tattatgaca 1200
aaactaaatc cttctttgat aatatttctt gtgatgacaa tagagaacgg agaccaacct 1260
gggctgaaga aagaagatta aatgctgaaa catttggaat ccacttctc ccaaaccgtg 1320
gccgtggggg atacagaggc agaggaggtc ttggtttccg tgggtggcaga gggcgtgggtg 1380
gtggcagagg tggtagcttc actgcccctc gaggatttcc cggtggattc agaggaggtc 1440
gtggggggccg ggagtttgcg gatttttgaat ataggaaaaac cacagctttt ggaccctaaa 1500
aggtctggat tgatcgact gctttctgaa agaaagacaa caaagttgct gcatagtcta 1560
caaacaagtc tctgaaaata ggtgaatttc tagctcttca tggctcctgaa cattgatctc 1620
agtctttgca aagaatgaag aagtgaattc gctgtacatt tgtcaccagc actgggtttt 1680
tgttttttgt ttgtttttcc gcttaatttc aaagataaaa tgcagttact tttgggggtg 1740
gaaggctcat cttaaaacat gagcattaaa tatatttgga atagcagaag gttaagtaat 1800
ttcttatgta tagttaaact aaagcagtac ttcagtggga cttaacaagt attttttcat 1860
cactgaaagg ttgttttttt tttatcacta aattgtattt ggcaattgca agttgcctgc 1920
agatagggcc gtgatactgt gttttgagcc acagaagggt gtgtgtgtgt gtgtgtgtgt 1980
gtgtgtgtgt gtgtgtgtgt gtatgtgtgt gtctttttcc tcctttcttt tggggaatcc 2040
tgtaatatga ggtagcttat ttcgtcaatt aattaggggt ctggatggta gagaattttg 2100
tcagtcaact atgtacacac agtaaatact gtttcttagg caaaggtaac ttttttatat 2160
agttgtaaaa ttccattata ttccattgcc aaagaaacat taagaccttt gtatagctgt 2220
ataaaaagca actaattttt taaagaaata aacattttta agtccaaaaa aaaaaaaaaa 2280
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2340
aaaaaaaaa aaaaaaaaaa aaaa 2364

```

&lt;210&gt; 16

&lt;211&gt; 463

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

```

Met Ser Gly Gly Thr Pro Tyr Ile Gly Ser Lys Ile Ser Leu Ile Ser
  1             5             10             15

```

```

Lys Ala Glu Ile Arg Tyr Glu Gly Ile Leu Tyr Thr Ile Asp Thr Glu
      20             25             30

```

```

Asn Ser Thr Val Ala Leu Ala Lys Val Arg Ser Phe Gly Thr Glu Asp
      35             40             45

```

```

Arg Pro Thr Asp Arg Pro Ile Pro Pro Arg Asp Glu Val Phe Glu Tyr
      50             55             60

```

```

Ile Ile Phe Arg Gly Ser Asp Ile Lys Asp Leu Thr Val Cys Glu Pro
      65             70             75             80

```

```

Pro Lys Pro Gln Cys Ser Leu Pro Gln Asp Pro Ala Ile Val Gln Ser
      85             90             95

```

```

Ser Leu Gly Ser Ser Thr Ser Ser Phe Gln Ser Met Gly Ser Tyr Gly
      100            105            110

```

```

Pro Phe Gly Arg Met Pro Thr Tyr Ser Gln Phe Ser Pro Ser Ser Leu
      115            120            125

```

```

Val Gly Gln Gln Phe Gly Ala Val Gly Val Ala Gly Ser Ser Leu Thr
      130            135            140

```

Ser Phe Gly Thr Glu Thr Ser Asn Ser Gly Thr Leu Pro Gln Ser Ser  
 145 150 155 160  
 Ala Val Gly Ser Ala Phe Thr Gln Asp Thr Arg Ser Leu Lys Thr Gln  
 165 170 175  
 Leu Ser Gln Gly Arg Ser Ser Pro Gln Leu Asp Pro Leu Arg Lys Ser  
 180 185 190  
 Pro Thr Met Glu Gln Ala Val Gln Thr Ala Ser Ala His Leu Pro Ala  
 195 200 205  
 Pro Ala Ala Val Gly Arg Arg Ser Pro Val Ser Thr Arg Pro Leu Pro  
 210 215 220  
 Ser Ala Ser Gln Lys Ala Gly Glu Asn Gln Glu His Arg Gln Ala Glu  
 225 230 235 240  
 Val His Lys Val Ser Arg Pro Glu Asn Glu Gln Leu Arg Asn Asp Asn  
 245 250 255  
 Lys Arg Gln Val Ala Pro Gly Ala Pro Ser Ala Pro Arg Arg Gly Arg  
 260 265 270  
 Gly Gly His Arg Gly Gly Arg Gly Arg Phe Gly Ile Arg Arg Asp Gly  
 275 280 285  
 Pro Met Lys Phe Glu Lys Asp Phe Asp Phe Glu Ser Ala Asn Ala Gln  
 290 295 300  
 Phe Asn Lys Glu Glu Ile Asp Arg Glu Phe His Asn Lys Leu Lys Leu  
 305 310 315 320  
 Lys Glu Asp Lys Leu Glu Lys Gln Glu Lys Pro Val Asn Gly Glu Asp  
 325 330 335  
 Lys Gly Asp Ser Gly Val Asp Thr Gln Asn Ser Glu Gly Asn Ala Asp  
 340 345 350  
 Glu Glu Asp Pro Leu Gly Pro Asn Cys Tyr Tyr Asp Lys Thr Lys Ser  
 355 360 365  
 Phe Phe Asp Asn Ile Ser Cys Asp Asp Asn Arg Glu Arg Arg Pro Thr  
 370 375 380  
 Trp Ala Glu Glu Arg Arg Leu Asn Ala Glu Thr Phe Gly Ile Pro Leu  
 385 390 395 400  
 Arg Pro Asn Arg Gly Arg Gly Gly Tyr Arg Gly Arg Gly Gly Leu Gly  
 405 410 415  
 Phe Arg Gly Gly Arg Gly Arg Gly Gly Gly Arg Gly Gly Thr Phe Thr  
 420 425 430  
 Ala Pro Arg Gly Phe Arg Gly Gly Phe Arg Gly Gly Arg Gly Gly Arg  
 435 440 445  
 Glu Phe Ala Asp Phe Glu Tyr Arg Lys Thr Thr Ala Phe Gly Pro  
 450 455 460

<210> 17  
 <211> 2760  
 <212> DNA  
 <213> Homo sapiens

<400> 17

```

tgaagatgcc tcctctgatg cctactgctt tgagctgctc tctatggttt tagcactgag 60
tggctctaac gttggccggc aatatctggc tcaacagcta accctgcttc aggatctctt 120
ctcgtctgctt cacacagcct ctctagagt ccagagacag gtaacctctt tactaagaag 180
agttttgcct gaagtaaccc ctagtctgtc ggccagcatc ataggagtga aatccctccc 240
cccagcagat atcagtgata tcattcactc aacagagaaa ggagactgga ataagctggg 300
tatcttggac atgtttctag gatgcattgc caaagcactc actgtacagc taaaagccaa 360
aggaaccacc atcactggaa cagctgggtac cactgtgggc aaaggagtta caacagttac 420
tcttccgatg attttcaatt ccagttatct ccgacgaggt gaaagtcatt ggtggatgaa 480
gggctcaacc cctaccaga tctcagagat catcattaaa cttatcaagg atatggcagc 540
aggtcatctg tcagaagctt ggtcccgagt gacaaaaaat gctattgcag aaaccatcat 600
tgccttgacc aagatggaag aagaatttag gtctccagtg agatgtattg caacaactag 660
actctggctt gctctcgcat ccctatgtgt tcttgatcag gaccacgtag atcgtctctc 720
ctcggggaga tggatgggaa aggatggaca acaaaaaaaa atgcctatgt gtgataacca 780
tgatgatggt gaaactgcag caatcatttt atgcaatgtc tgtggaaatt tatgtacaga 840
ctgtgacaga ttcttccacc ttcatcgaag aacccaaact catcaaagac aggtcttcaa 900
agaagaagaa gaagctataa aggttgacct tcatgaaggt tgtggtagaa ccaaattgtt 960
ctggttgatg gactggcag attctaaaac aatgaaggca atggtggaat tccgagaaca 1020
cacaggcaaa cccaccacga gtagctcaga agcatgtcgc ttctgtggtt ccaggagtgg 1080
aacagagtta tctgctgttg gcagtgtttg ttctgatgca gattgccagg aatacgctaa 1140
gatagcctgt agtaagacgc atccttgttg ccattccatgc gggggtgtta aaaacgaaga 1200
gactgtctg ccctgtctac acggctgtga caaaagtgc acaagcctga agcaagacgc 1260
cgatgacatg tgcatgatat gtttcaccga agcgtctctg gcagcaccag ccattcagct 1320
ggattgtagt cacatattcc acttacagtg ctgtcggcga gtattagaaa atcgatggct 1380
tggcccaagg ataactttg gatattatc ttgtcccat tgcagaaca aaattaatca 1440
catagtacta aaagacctac ttgatccaat aaaagaactc tatgaggatg tcagaagaaa 1500
agccttaatg agattggaat atgaaggtct gcataagagt gaagctatca caactcctgg 1560
tgtgaggttt tataatgacc cagctggcta tgcaatgaat agatatgcat attatgtgtg 1620
ctacaaatgc agaaaggcat attttgggtg tgaagctcgc tgcgatgctg aggctggacg 1680
gggagatgat tatgatccca gagagctcat ttgtggtgcc tgttctgatg ttccagggc 1740
tcagatgtgt cccaaacatg gcacagactt ttggaatat aaatgtcgt actgctgttc 1800
agtggctgtt tttttctgtt ttggaacaac acatttttgt aatgcttgtc atgatgattt 1860
tcaaagaatg actagcattc ctaaggaaga actaccacac tgtcctgcag gtcccaaagg 1920
caagcagtta gaaggaactg aatgtccact ccattgttgt catccacca ctggggaaga 1980
gtttgtctg gtagtggtgag tgtgcagaaa tgccacact ttttagaaca cgcagatcct 2040
ttgtctacag agagaaaaat tgccttcac cccaagagg atgcggtgaa gtttaactc 2100
tgctcaggat aaggacggga ccatttttac atccatgaaa atgaaccatt cacagtgcaa 2160
gaaggatacc aaataccatg tacataattc ttgctatgaa agttttcccc attatttttg 2220
tttatcttct tttgaacaaa tgacatcaaa cttgtgaggt gtttgcattg ggccattacc 2280
gtcattggcc tgtgaagcat tggacattta tagataattg atataaaaga atcgccatgc 2340
ccatggacta agaacgatgc tggctttcaa gcaaaaaaga aaaataatca ttgtttattg 2400
tatactgcct ttttgaatc ctgtacaatt gcatcacggg tggggataaa aagaggaata 2460
ttctggttta ttctctagac tgttatttaa aaaaaaaaaa acattgtgtt aggacagcat 2520
ataaatgtaa taagtatcac actgtatata aacatatcaa tgtttgtcct gtataagaat 2580
tactaaatta caaatgcaat ttcatttaaa cttctagggt aagtttgagc ctgaaatatt 2640
aatgaagtgc aatactgagt gtgcctcatt atcttgcagc tgtaaacata ttggaatgta 2700
catgtcaata aaaccactgt acatttttat acagtgataa agtctaaaaa aaaaaaaaaa 2760

```

<210> 18  
 <211> 660  
 <212> PRT  
 <213> Homo sapiens

<400> 18

Met Val Leu Ala Leu Ser Gly Ser Asn Val Gly Arg Gln Tyr Leu Ala  
 1 5 10 15  
 Gln Gln Leu Thr Leu Leu Gln Asp Leu Phe Ser Leu Leu His Thr Ala  
 20 25 30  
 Ser Pro Arg Val Gln Arg Gln Val Thr Ser Leu Leu Arg Arg Val Leu  
 35 40 45  
 Pro Glu Val Thr Pro Ser Arg Leu Ala Ser Ile Ile Gly Val Lys Ser  
 50 55 60  
 Leu Pro Pro Ala Asp Ile Ser Asp Ile Ile His Ser Thr Glu Lys Gly  
 65 70 75 80  
 Asp Trp Asn Lys Leu Gly Ile Leu Asp Met Phe Leu Gly Cys Ile Ala  
 85 90 95  
 Lys Ala Leu Thr Val Gln Leu Lys Ala Lys Gly Thr Thr Ile Thr Gly  
 100 105 110  
 Thr Ala Gly Thr Thr Val Gly Lys Gly Val Thr Thr Val Thr Leu Pro  
 115 120 125  
 Met Ile Phe Asn Ser Ser Tyr Leu Arg Arg Gly Glu Ser His Trp Trp  
 130 135 140  
 Met Lys Gly Ser Thr Pro Thr Gln Ile Ser Glu Ile Ile Ile Lys Leu  
 145 150 155 160  
 Ile Lys Asp Met Ala Ala Gly His Leu Ser Glu Ala Trp Ser Arg Val  
 165 170 175  
 Thr Lys Asn Ala Ile Ala Glu Thr Ile Ile Ala Leu Thr Lys Met Glu  
 180 185 190  
 Glu Glu Phe Arg Ser Pro Val Arg Cys Ile Ala Thr Thr Arg Leu Trp  
 195 200 205  
 Leu Ala Leu Ala Ser Leu Cys Val Leu Asp Gln Asp His Val Asp Arg  
 210 215 220  
 Leu Ser Ser Gly Arg Trp Met Gly Lys Asp Gly Gln Gln Lys Gln Met  
 225 230 235 240  
 Pro Met Cys Asp Asn His Asp Asp Gly Glu Thr Ala Ala Ile Ile Leu  
 245 250 255  
 Cys Asn Val Cys Gly Asn Leu Cys Thr Asp Cys Asp Arg Phe Leu His  
 260 265 270  
 Leu His Arg Arg Thr Lys Thr His Gln Arg Gln Val Phe Lys Glu Glu  
 275 280 285  
 Glu Glu Ala Ile Lys Val Asp Leu His Glu Gly Cys Gly Arg Thr Lys  
 290 295 300  
 Leu Phe Trp Leu Met Ala Leu Ala Asp Ser Lys Thr Met Lys Ala Met  
 305 310 315 320

Val Glu Phe Arg Glu His Thr Gly Lys Pro Thr Thr Ser Ser Ser Glu  
 325 330 335  
 Ala Cys Arg Phe Cys Gly Ser Arg Ser Gly Thr Glu Leu Ser Ala Val  
 340 345 350  
 Gly Ser Val Cys Ser Asp Ala Asp Cys Gln Glu Tyr Ala Lys Ile Ala  
 355 360 365  
 Cys Ser Lys Thr His Pro Cys Gly His Pro Cys Gly Gly Val Lys Asn  
 370 375 380  
 Glu Glu His Cys Leu Pro Cys Leu His Gly Cys Asp Lys Ser Ala Thr  
 385 390 395 400  
 Ser Leu Lys Gln Asp Ala Asp Asp Met Cys Met Ile Cys Phe Thr Glu  
 405 410 415  
 Ala Leu Ser Ala Ala Pro Ala Ile Gln Leu Asp Cys Ser His Ile Phe  
 420 425 430  
 His Leu Gln Cys Cys Arg Arg Val Leu Glu Asn Arg Trp Leu Gly Pro  
 435 440 445  
 Arg Ile Thr Phe Gly Phe Ile Ser Cys Pro Ile Cys Lys Asn Lys Ile  
 450 455 460  
 Asn His Ile Val Leu Lys Asp Leu Leu Asp Pro Ile Lys Glu Leu Tyr  
 465 470 475 480  
 Glu Asp Val Arg Arg Lys Ala Leu Met Arg Leu Glu Tyr Glu Gly Leu  
 485 490 495  
 His Lys Ser Glu Ala Ile Thr Thr Pro Gly Val Arg Phe Tyr Asn Asp  
 500 505 510  
 Pro Ala Gly Tyr Ala Met Asn Arg Tyr Ala Tyr Tyr Val Cys Tyr Lys  
 515 520 525  
 Cys Arg Lys Ala Tyr Phe Gly Gly Glu Ala Arg Cys Asp Ala Glu Ala  
 530 535 540  
 Gly Arg Gly Asp Asp Tyr Asp Pro Arg Glu Leu Ile Cys Gly Ala Cys  
 545 550 555 560  
 Ser Asp Val Ser Arg Ala Gln Met Cys Pro Lys His Gly Thr Asp Phe  
 565 570 575  
 Leu Glu Tyr Lys Cys Arg Tyr Cys Cys Ser Val Ala Val Phe Phe Cys  
 580 585 590  
 Phe Gly Thr Thr His Phe Cys Asn Ala Cys His Asp Asp Phe Gln Arg  
 595 600 605  
 Met Thr Ser Ile Pro Lys Glu Glu Leu Pro His Cys Pro Ala Gly Pro  
 610 615 620  
 Lys Gly Lys Gln Leu Glu Gly Thr Glu Cys Pro Leu His Val Val His  
 625 630 635 640

Pro Pro Thr Gly Glu Glu Phe Ala Leu Gly Cys Gly Val Cys Arg Asn  
 645 650 655

Ala His Thr Phe  
 660

<210> 19  
 <211> 1649  
 <212> DNA  
 <213> Homo sapiens

<400> 19  
 gattgtacat agtcttgtgg ggcattggggg agccggctgg aggtgagaac cctccccctct 60  
 cccccacccc cccgggggaga gcaaatgtaa aactactaat ttttgtgctt tatatatctt 120  
 atataaatat atctattttc tttttacaaa accagtttat aaatggtagg ggggtgtggg 180  
 gcggacacat ggagctcccc ttgtgggggg gccccctcca ttaccgacc taccgccctt 240  
 ttcttcacccc cccaccccac tccccacccc ctggctgtga ctgctgtaag atgggggtat 300  
 agaggctggg caattcccac cccctgttgt atagttggac tatgttataa cgcacaaaag 360  
 agagctgacc ccagggggag ccagagggtg atgggttcct tgcctccctt tccttcccc 420  
 ttttgcctaa gcttgtgctg cagtgaacc tcttctggg ggtgggagta ggtaaggggt 480  
 ggggtaggcc ccaaacccct ctctggtagg gaaccgtggg gatgaagatg aagcttatat 540  
 gcagttctct tctaggggct gtgggcaaag ggcattttgt aattaatatt ttcaagaatc 600  
 agatgtcttg agtgtagggg tgggcttggg ggtgggtggc gggcgggcct gctggagggg 660  
 gagcttggtc gctgttgtga ttttaggttt gtttttgttt tgttttgaat ttgggggggt 720  
 gtggattggt gggggtaggg agattttttt ttttttaaag ctgcttcctc aactgtttca 780  
 agctgcaaat gtttaagaga ataacagccc ccactcccac aggaaccgct gtaattaaat 840  
 cagacagtag gaagactggg ctgctgccct caaagccaca gcccttggat gttccttttc 900  
 cgagagcaga aggtctaggc tacaggaggg gggagattgg ctcccgtgag tcaggctgtg 960  
 tttggggctt gggccctggg attgggaaaa ggggatgggg cagactttgt aagcatatgc 1020  
 taggtatccg atagtcctgt agaatttagt gaagaaacct tatacagttt ttaattttta 1080  
 tataaactat aactcagacc caagctacaa ggttggaatt ttggttgggt ttttttttaa 1140  
 gtaccctgcc tgtataattg catcagaatc cccaccccca ccccsgcc csgtgtttgt 1200  
 attttgggtt ggtttacact cgcacatact cagttttcag ttttccccct tacagtcttc 1260  
 tccccacacc tccaggaccc tccccctttt taaaaataaa atcgctgaca agtgtgaatc 1320  
 ccgtgaagac tttattttgt gttgtgtgta tctgtacag caaggttggg ccttcgtaac 1380  
 aacggatgaa atggttcctt tttttaaaag gccctctctc cctccaccct cagcgccctt 1440  
 gtccttgga tgttttgtat cagcgatcat tctgaactgt acataattat gttgcgagag 1500  
 gcaaggggca agttttggat tttgcttctt ccaagtttgt ttttaaacga caaataaaaa 1560  
 aagaacattt taaataaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1620  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1649

<210> 20  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Met Gly Glu Pro Ala Gly Gly Glu Asn Pro Pro Leu Ser Pro His Pro  
 1 5 10 15  
 Pro Gly Arg Ala Asn Val Lys Leu Leu Ile Phe Val Leu Tyr Ile Phe  
 20 25 30  
 Tyr Ile Asn Ile Ser Ile Phe Phe Leu Gln Asn Gln Phe Ile Asn Gly  
 35 40 45  
 Arg Gly Val Trp Gly Gly His Met Glu Leu Pro Leu Trp Gly Gly Pro  
 50 55 60

Leu His Tyr Pro Thr Tyr Arg Pro Phe Pro His Pro Pro Pro His Ser  
 65 70 75 80

Pro Pro Pro Gly Cys Asp Cys Cys Lys Met Gly Val  
 85 90

<210> 21  
 <211> 2644  
 <212> DNA  
 <213> Homo sapiens

<400> 21  
 gttgaggatg gctgacattc tctctcagtc agagaccctg gcgtcgcaag acctcagtgg 60  
 ggacttcaag aagccagctc tgccgggtgtc cccagcggcg cggagtaagg ccccgccag 120  
 cagttcttca aacctgagg aggtacagaa ggaagggccc actgcgttgc aggactccaa 180  
 ttctggggag cccgacatcc ctctcctca gccggactgc ggtgatttta ggagtctaca 240  
 ggaggagcag tcgcgcccca cgacagcggg ttcttcccct ggcggtccag cccgggctcc 300  
 cccctaccaaa gagcctccat ggggtggccc tgccacagcc ccctacagct tagagaccct 360  
 gaagggcggc actatccttg gcaccgtag cttgaaaggg acgagttact gccttttcgg 420  
 gaggctgtct ggctgcgacg tgtgcctgga gcacccttcg gtgtctcggg accacgcagt 480  
 gctgcagcac agggcgctccg gccctgacgg agaatgcgac agcaacgggc cgggcttcta 540  
 cctctacgat ctgggaagca cccatggcac tttctcaaac aaaactcgca tcccacctcg 600  
 cactactgt cgagtccacg ttgggcatgt tgttcgcttt ggaggcagca cccggctctt 660  
 tatcctgcag ggaccagagg aagaccgaga ggcagaatcc gagttaacag taacacagtt 720  
 gaaggaattg cgcaagcagc agcaaatatt gttggrgaag aagatgctag gagaagactc 780  
 agatgaagaa gaggaaatgg atacctctga aaggaagata aatgctggta gccaaagatga 840  
 tgagatgggt tgcacctggg gaatgggaga agatgcagta gaggatgatg ctgaagagaa 900  
 ccctattgtc ttagagtttc agcaggaaa ggaggccttt tatataaagg atcccaaaaa 960  
 ggctctccaa ggcttttttg accgagaagg agaagaatta gaatatgaat ttgatgaaca 1020  
 gggacatagc acttggctct gcagggtgag attacctgtg gacgattcaa ctggaaaaca 1080  
 actggtggct gaggccattc actcaggaaa gaaaaaagaa gcaatgatcc agtgctcatt 1140  
 ggaagcttgt cggattcttg acactttggg attgcttcgg caggaaagcag tatctcggaa 1200  
 aaggaaagcc aagaactggg aagatgaaga cttttatgat agtgatgatg acacatttct 1260  
 tgataggact ggcctgattg agaagaagcg tctgaacaga atgaagaagg ctggcaagat 1320  
 tgatgagaag ccagagacct ttgaatcatt ggttgcaaaa ttaaatgatg ctgaaagggg 1380  
 actttctgaa atttctgaga gattgaaagc ctcaagccaa gttctatcag agtctccatc 1440  
 tcaggattct ttagatgcgt tcattgtcaga aatgaaatca ggcagtacat tagatgggtg 1500  
 gtcccggaag aaacttcacc tgagaacttt tgaactgagg aaagaacaac agagacttaa 1560  
 agggtaataa aaaattgtaa agccagcaga gattccagaa ctaaaaaaga ctgaaactca 1620  
 gactacaggt gcagaaaaca aagctaaaaa gcttacattg cctctatttg gtgccatgaa 1680  
 aggaggaagc aaattcaaat taaaaactgg aacagtaggg aagttacccc ccaagcgtcc 1740  
 agaactccct ccaactctaa tgagaatgaa agatgagcct gaagtagaag aggaggagga 1800  
 agaggaagag gaagaagaga aagaaaagga ggagcatgaa aagaaaaaac tggaggatgg 1860  
 aagcctcagt aggccacagc cagagataga gccagaagca gcagtgcagg aaatgaggcc 1920  
 tcccacagat ctacacatt ttaaagaaac ccaaaccat ggtaatatct ttcttctcct 1980  
 tcctgtgttg ttcagtgggc agttacattg attgtggata ggttttaaaa agcaaggcca 2040  
 gttcttgtct gtgcatttga cttgttatgt gatatactga ctctgtagca aggaaacata 2100  
 ctttcttggg cttcttcctt tgaccgccag tcattatttg tcttcattgc aaattaaggg 2160  
 cagttatttc caatccattc cagaattaca gaaaattgaa gggctatgga atctgaaacc 2220  
 atagctgtcg tggaataatc ctgagctgct gccactgtgt gaggttggagg gcagtgggaa 2280  
 aggggtacatg atggggcctg atcagggtgt ctccggataa gtcaacccct attcattttt 2340  
 tcctccatcc ctaaaacaga ggccaaacca taattgtact cattggacta aagttctcaa 2400  
 gaaggatctt gcttcattca tttttgtgtg ttgtgaaact agcacaacac ctgacacata 2460  
 tcccccgcgc tcagcaaata tttgatgaaa aatgttgaaa gacggaaatag attgatattc 2520  
 atatagatat atgcatcaat taattctgta ttttctatat atatattcta attacaaagg 2580  
 gttatatgtt cattttagaa actatagatc atacataaaa gtccaaagga aaaaaaaaaa 2640  
 aaaa 2644

<210> 22



<211> 667  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (250)

<400> 22

Met Ala Asp Ile Leu Ser Gln Ser Glu Thr Leu Ala Ser Gln Asp Leu  
 1 5 10 15

Ser Gly Asp Phe Lys Lys Pro Ala Leu Pro Val Ser Pro Ala Ala Arg  
 20 25 30

Ser Lys Ala Pro Ala Ser Ser Ser Ser Asn Pro Glu Glu Val Gln Lys  
 35 40 45

Glu Gly Pro Thr Ala Leu Gln Asp Ser Asn Ser Gly Glu Pro Asp Ile  
 50 55 60

Pro Pro Pro Gln Pro Asp Cys Gly Asp Phe Arg Ser Leu Gln Glu Glu  
 65 70 75 80

Gln Ser Arg Pro Thr Thr Ala Val Ser Ser Pro Gly Gly Pro Ala Arg  
 85 90 95

Ala Pro Pro Tyr Gln Glu Pro Pro Trp Gly Gly Pro Ala Thr Ala Pro  
 100 105 110

Tyr Ser Leu Glu Thr Leu Lys Gly Gly Thr Ile Leu Gly Thr Arg Ser  
 115 120 125

Leu Lys Gly Thr Ser Tyr Cys Leu Phe Gly Arg Leu Ser Gly Cys Asp  
 130 135 140

Val Cys Leu Glu His Pro Ser Val Ser Arg Tyr His Ala Val Leu Gln  
 145 150 155 160

His Arg Ala Ser Gly Pro Asp Gly Glu Cys Asp Ser Asn Gly Pro Gly  
 165 170 175

Phe Tyr Leu Tyr Asp Leu Gly Ser Thr His Gly Thr Phe Leu Asn Lys  
 180 185 190

Thr Arg Ile Pro Pro Arg Thr Tyr Cys Arg Val His Val Gly His Val  
 195 200 205

Val Arg Phe Gly Gly Ser Thr Arg Leu Phe Ile Leu Gln Gly Pro Glu  
 210 215 220

Glu Asp Arg Glu Ala Glu Ser Glu Leu Thr Val Thr Gln Leu Lys Glu  
 225 230 235 240

Leu Arg Lys Gln Gln Gln Ile Leu Leu Xaa Lys Lys Met Leu Gly Glu  
 245 250 255

Asp Ser Asp Glu Glu Glu Glu Met Asp Thr Ser Glu Arg Lys Ile Asn  
 260 265 270

Ala Gly Ser Gln Asp Asp Glu Met Gly Cys Thr Trp Gly Met Gly Glu  
 275 280 285  
 Asp Ala Val Glu Asp Asp Ala Glu Glu Asn Pro Ile Val Leu Glu Phe  
 290 295 300  
 Gln Gln Glu Arg Glu Ala Phe Tyr Ile Lys Asp Pro Lys Lys Ala Leu  
 305 310 315 320  
 Gln Gly Phe Phe Asp Arg Glu Gly Glu Glu Leu Glu Tyr Glu Phe Asp  
 325 330 335  
 Glu Gln Gly His Ser Thr Trp Leu Cys Arg Val Arg Leu Pro Val Asp  
 340 345 350  
 Asp Ser Thr Gly Lys Gln Leu Val Ala Glu Ala Ile His Ser Gly Lys  
 355 360 365  
 Lys Lys Glu Ala Met Ile Gln Cys Ser Leu Glu Ala Cys Arg Ile Leu  
 370 375 380  
 Asp Thr Leu Gly Leu Leu Arg Gln Glu Ala Val Ser Arg Lys Arg Lys  
 385 390 395 400  
 Ala Lys Asn Trp Glu Asp Glu Asp Phe Tyr Asp Ser Asp Asp Asp Thr  
 405 410 415  
 Phe Leu Asp Arg Thr Gly Leu Ile Glu Lys Lys Arg Leu Asn Arg Met  
 420 425 430  
 Lys Lys Ala Gly Lys Ile Asp Glu Lys Pro Glu Thr Phe Glu Ser Leu  
 435 440 445  
 Val Ala Lys Leu Asn Asp Ala Glu Arg Glu Leu Ser Glu Ile Ser Glu  
 450 455 460  
 Arg Leu Lys Ala Ser Ser Gln Val Leu Ser Glu Ser Pro Ser Gln Asp  
 465 470 475 480  
 Ser Leu Asp Ala Phe Met Ser Glu Met Lys Ser Gly Ser Thr Leu Asp  
 485 490 495  
 Gly Val Ser Arg Lys Lys Leu His Leu Arg Thr Phe Glu Leu Arg Lys  
 500 505 510  
 Glu Gln Gln Arg Leu Lys Gly Leu Ile Lys Ile Val Lys Pro Ala Glu  
 515 520 525  
 Ile Pro Glu Leu Lys Lys Thr Glu Thr Gln Thr Thr Gly Ala Glu Asn  
 530 535 540  
 Lys Ala Lys Lys Leu Thr Leu Pro Leu Phe Gly Ala Met Lys Gly Gly  
 545 550 555 560  
 Ser Lys Phe Lys Leu Lys Thr Gly Thr Val Gly Lys Leu Pro Pro Lys  
 565 570 575  
 Arg Pro Glu Leu Pro Pro Thr Leu Met Arg Met Lys Asp Glu Pro Glu  
 580 585 590

Val Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Lys Glu Lys Glu  
 595 600 605

Glu His Glu Lys Lys Lys Leu Glu Asp Gly Ser Leu Ser Arg Pro Gln  
 610 615 620

Pro Glu Ile Glu Pro Glu Ala Ala Val Gln Glu Met Arg Pro Pro Thr  
 625 630 635 640

Asp Leu Thr His Phe Lys Glu Thr Gln Thr His Gly Asn Ile Phe Leu  
 645 650 655

Leu Leu Pro Val Leu Phe Ser Gly Gln Leu His  
 660 665

<210> 23  
 <211> 2402  
 <212> DNA  
 <213> Homo sapiens

<400> 23

gatcgagag accaaggagg cgcccgcggc tgcagagctg cagagcgagg tctcttcgag 60  
 ctgtctgtgt ccgggcagcc ggcgcgcaac tgagccagag gacagcgcat ccttttcggcg 120  
 cgggccggca gggcccttgc gggtcgcaag ctggctcccc ggggtggccac cgggaccccc 180  
 gagcccaatg gcgggggagg cggaacaaatc cacaacactg tagagatcac ccccacctcc 240  
 aacgggacagg tcgggaccct cggagatgag gtgcccacgg agcagctgca gggtagcgag 300  
 gagcgcgagc gggaggggga gggagacgag ggcgggcgag gactgggagc cagcctgtcg 360  
 ctggccgtgc cccagggccc cctcagcttt tgctgcctgc cggtgctctt cgtggctctg 420  
 ggcgggcgcc agcagctgca gctcggcctc tgctgcctgc cggtgctctt cgtggctctg 480  
 ggcatggcct cggaccccat cttcacgctg gcgccccgcg tgcattgcca ctacggggcc 540  
 ttcccccta atgcctctgg ctgggagcag cctcccaatg ccagcgcggt cagcgtcgcc 600  
 agcgtgccc tagcagccag cgccgccagc cgtgtcgcca ccagtaccga cccctcgtgc 660  
 agcggtctcg ccccgccgga cttcaaccat tgcctcaagg attgggacta taatggcctt 720  
 cctgtgtcca ccaccaacgc catcgccagc tgggatctgg tgtgtgacct gggctggcag 780  
 gtgacctcgg agcagatcct cttcatcttg ggctttgcct ccggctacct gttcctgggt 840  
 taccgagcag acagatttgg ccgtcgcggg attgtgctgc tgacctggg gctgggtggg 900  
 cctgtggag taggaggggc tgctgcaggc tcctccacag gcgtcatggc cctccgatte 960  
 ctcttgggct ttctgcttgc cgggtgtgac ctgggtgtct acctgatgcg cctggagctg 1020  
 tgcgacccaa cccagaggct tcgggtggcc ctggcagggg agttgggtggg ggtgggaggg 1080  
 cacttctctg tcctgggcct ggcccttctc tctaaggatt ggcgattcct acagcgaatg 1140  
 atcaccgctc cctgcaccc cttcctgttt tatggctggc ctgggttgtt cctggagtcc 1200  
 gcacgggtgg tgatagtga gggcgagatt gaggaggctc agtctgtgct gaggatcctg 1260  
 gctgagcgaa accggcccca tgggcagatg ctgggggagg agggccagga ggccctgcag 1320  
 gacctggaga atacctgccc tctccctgca acatcctcct ttctcttgc ttccctcctc 1380  
 aactaccgca acatctggaa aaatctgctt atcctgggct tcaccaactt cattgcccc 1440  
 gccattcgcc actgctacca gcctgtggga ggaggaggga gcccatcgga cttctacctg 1500  
 tgctctctgc tggccagcgg caccgcagcc ctggcctgtg tcttctctggg ggtcaccgtg 1560  
 gaccgatttg gccgcccggg catccttctt ctctccatga cccttaccgg cattgcttcc 1620  
 ctggctcctg tgggcctgtg ggattatctg aacgaggctg ccatcaccac tttctctgtc 1680  
 cttgggctct tctcctccca agctgcggcc atcctcagca ccctccttgc tgctgaggtc 1740  
 atccccacca ctgtccgggg ccgtggcctg ggcctgatca tggctctagg ggcgcttgga 1800  
 ggagtggcgg gcccgcccca gcgcctccac atgggcatg gagccttctt gcagcacgtg 1860  
 gtgctggcgg cctgcgcctt cctctgcatt ctacagatta tgctgctgac ggagaccaag 1920  
 cgcaagctcc tgcccagggt gctccgggac ggggagctgt gtcgcccggc ttccctgtcg 1980  
 cggcagccac cccctaccgg ctgtgaccac gtcccgtgct ttgccacccc caacctgccc 2040  
 ctctgagcgg cctctgagta ccctggcggg aggctggccc acacagaaag gtggcaagaa 2100  
 gatcggggag actgagtagg gaaggcaggg ctgcccagaa gtctcagagg cacctcacgc 2160  
 cagccatcgc ggagagctca gagggccgtc cccacctgct ctctcctctg ctgcttttgc 2220  
 ttcacttctt tggccagagt caggggacag ggagagagct ccacactgta accactgggt 2280

ctgggctcca tcctgcgccc aaagacatcc acccagacct cattatttct tgctctatca 2340  
 ttctgtttca ataaagacat ttggaataaa cgaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2400  
 aa 2402

<210> 24

<211> 520

<212> PRT

<213> Homo sapiens

<400> 24

Met Ala Ser Asp Pro Ile Phe Thr Leu Ala Pro Pro Leu His Cys His  
 1 5 10 15

Tyr Gly Ala Phe Pro Pro Asn Ala Ser Gly Trp Glu Gln Pro Pro Asn  
 20 25 30

Ala Ser Gly Val Ser Val Ala Ser Ala Ala Leu Ala Ala Ser Ala Ala  
 35 40 45

Ser Arg Val Ala Thr Ser Thr Asp Pro Ser Cys Ser Gly Phe Ala Pro  
 50 55 60

Pro Asp Phe Asn His Cys Leu Lys Asp Trp Asp Tyr Asn Gly Leu Pro  
 65 70 75 80

Val Leu Thr Thr Asn Ala Ile Gly Gln Trp Asp Leu Val Cys Asp Leu  
 85 90 95

Gly Trp Gln Val Ile Leu Glu Gln Ile Leu Phe Ile Leu Gly Phe Ala  
 100 105 110

Ser Gly Tyr Leu Phe Leu Gly Tyr Pro Ala Asp Arg Phe Gly Arg Arg  
 115 120 125

Gly Ile Val Leu Leu Thr Leu Gly Leu Val Gly Pro Cys Gly Val Gly  
 130 135 140

Gly Ala Ala Ala Gly Ser Ser Thr Gly Val Met Ala Leu Arg Phe Leu  
 145 150 155 160

Leu Gly Phe Leu Leu Ala Gly Val Asp Leu Gly Val Tyr Leu Met Arg  
 165 170 175

Leu Glu Leu Cys Asp Pro Thr Gln Arg Leu Arg Val Ala Leu Ala Gly  
 180 185 190

Glu Leu Val Gly Val Gly Gly His Phe Leu Phe Leu Gly Leu Ala Leu  
 195 200 205

Val Ser Lys Asp Trp Arg Phe Leu Gln Arg Met Ile Thr Ala Pro Cys  
 210 215 220

Ile Leu Phe Leu Phe Tyr Gly Trp Pro Gly Leu Phe Leu Glu Ser Ala  
 225 230 235 240

Arg Trp Leu Ile Val Lys Arg Gln Ile Glu Glu Ala Gln Ser Val Leu  
 245 250 255

Arg Ile Leu Ala Glu Arg Asn Arg Pro His Gly Gln Met Leu Gly Glu  
 260 265 270

Glu Ala Gln Glu Ala Leu Gln Asp Leu Glu Asn Thr Cys Pro Leu Pro  
 275 280 285  
 Ala Thr Ser Ser Phe Ser Phe Ala Ser Leu Leu Asn Tyr Arg Asn Ile  
 290 295 300  
 Trp Lys Asn Leu Leu Ile Leu Gly Phe Thr Asn Phe Ile Ala His Ala  
 305 310 315 320  
 Ile Arg His Cys Tyr Gln Pro Val Gly Gly Gly Gly Ser Pro Ser Asp  
 325 330 335  
 Phe Tyr Leu Cys Ser Leu Leu Ala Ser Gly Thr Ala Ala Leu Ala Cys  
 340 345 350  
 Val Phe Leu Gly Val Thr Val Asp Arg Phe Gly Arg Arg Gly Ile Leu  
 355 360 365  
 Leu Leu Ser Met Thr Leu Thr Gly Ile Ala Ser Leu Val Leu Leu Gly  
 370 375 380  
 Leu Trp Asp Tyr Leu Asn Glu Ala Ala Ile Thr Thr Phe Ser Val Leu  
 385 390 395 400  
 Gly Leu Phe Ser Ser Gln Ala Ala Ala Ile Leu Ser Thr Leu Leu Ala  
 405 410 415  
 Ala Glu Val Ile Pro Thr Thr Val Arg Gly Arg Gly Leu Gly Leu Ile  
 420 425 430  
 Met Ala Leu Gly Ala Leu Gly Gly Leu Ser Gly Pro Ala Gln Arg Leu  
 435 440 445  
 His Met Gly His Gly Ala Phe Leu Gln His Val Val Leu Ala Ala Cys  
 450 455 460  
 Ala Leu Leu Cys Ile Leu Ser Ile Met Leu Leu Pro Glu Thr Lys Arg  
 465 470 475 480  
 Lys Leu Leu Pro Glu Val Leu Arg Asp Gly Glu Leu Cys Arg Arg Pro  
 485 490 495  
 Ser Leu Leu Arg Gln Pro Pro Pro Thr Arg Cys Asp His Val Pro Leu  
 500 505 510  
 Leu Ala Thr Pro Asn Pro Ala Leu  
 515 520

&lt;210&gt; 25

&lt;211&gt; 2377

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 25

ttcattcttc agtggaatc catcagttga aatagttcat ggtattatgc acctatataa 60  
 gacaaataag atgacctcct taaaagaaga tgtgcggcgc agtgccatgc tgtgtattct 120  
 cacagtcctt gctgcaatga ccagtcata ccttatgaag tttgttgccc catttaacga 180  
 agtaattgaa caaatgaaaa ttatcagaga ctctactccc aaccaatata tgggtctgat 240

```

aaagtttcgt gcacaggctg atgcggatag tttttatatg acatgcaatg gccgccagtt 300
caactcaata gaagatgacg tttgccagct agtgtatgtg gaaagagctg aagtgtctcaa 360
atctgaagat ggcgccagcc tcccagtgat ggacctgact gaactcccca agtgccaggt 420
gtgtctggag cgcattggacg agtctgtgaa tggcatcctc acaacgttat gtaaccacag 480
cttccacagc cagtgtctac agcgtctggga cgataccacg tgtcctgttt gccggtactg 540
tcaaacgccc gagccagtag aagaaaataa gtgttttgag tgtggtgttc aggaaaatct 600
ttggatttgt ttaatatgcg gccacatagg atgtggacgg tatgtcagtc gacatgctta 660
taagcacttt gaggaacgc agcacacgta tgccatgcag cttaccaacc atcgagtctg 720
ggactatgct ggagataact atgttcatcg actgggtgca agtaaaacag atggaaaaat 780
agtacagtat gaatgtgagg gggatacttg ccaggaagag aaaatagatg ccttacagtt 840
agagtattca tatttactaa caagccagct ggaatctcag cgaatctact gggaaaacaa 900
gatagtctcg atagagaagg acacagcaga ggaaattaac aacatgaaga ccaagttaa 960
agaaacaatt gagaagtgtg ataacttaga gcacaaacta aatgatctcc taaaagaaaa 1020
gcagtctgtg gaaagaaagt gcactcagct aaacacaaaa gtggccaaac tcaaatctca 1080
gagtgggtat cctagcatct agcaagactg agtggggaga tttctcatcc gtgtgaaaat 1140
gtagagttag gcctctgact agctaattgt gtattttgtt gggtttagta ttttctaaat 1200
gtttacaaaa tattgggctg catgttcagg ttgcagctag agggagcttg ggcagatttt 1260
caattacgct ttcaagatat aaccaaaagc tgtttctaaa tcctaaaatt agaatttcaa 1320
cagagccccc tttagaacag tcatataacg cttgtgtggg ccaacagagg ggctgtgtac 1380
tctctctgga accataaatg tcaaataatt tataacctgc agtaattgag caaacttaaa 1440
ataagacctg tgttgaatt tagtttcttg aagaggtaga gggatagggt agtaagatgt 1500
attgttaaac aacaggtttt agtttttgct ttataattag ccacagggtt tcaaattgatc 1560
acatttcaga ataggttttt agcctgtaat taggcctcat ccccttgac ctaaattgtct 1620
gacatgttac ttgttagcac atcaactgta tcactaatca ccatctgttt ttgtgggatg 1680
tgctgcagca tttcccaaaa aactttacgt gtaatgttgc aaaatgaatg tactcagaca 1740
ttcttaattt ttacttaggg cagaccaact ctttgagtct ctcttggaact tatatataca 1800
gatattctaa gagtgggaat gtaaagcata accttaattct ctttctata gagattctat 1860
tttatttaaa atctattttt acactagtta gaatcctgct gttttggcca agtactgttc 1920
ttgcatgtct gaccttgacg aagctggggt ggatcatagc atactaatga agagaattag 1980
aagtagttaa caaagctcgc tcaactctca tttctctgtg atcccttcta tccagtggcc 2040
ccaccaccac ctgggaaaac agatttttca gtacagggtg gataaatgct ttgaaaggct 2100
gtgcccagag caatgagcaa ataggcaagt gtttccaaac tamttggagg tttacaaaaa 2160
atatgtccca gaaaaaaaaa aaatcttacc aagataccta aagaaaaaaa aatttttttt 2220
taaacagtcg aagagtcag tttgaatttc acaaaatcac atcagacaga agttgttttc 2280
ttcaggaggg aaatgaacca cttaatatc ccatactacc ttgaacaatg aaattgaatt 2340
aaaatagcca aactttgaaa ttaaaaaaaaa aaaaaaa 2377

```

&lt;210&gt; 26

&lt;211&gt; 351

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 26

```

Met His Leu Tyr Lys Thr Asn Lys Met Thr Ser Leu Lys Glu Asp Val
  1             5             10             15

```

```

Arg Arg Ser Ala Met Leu Cys Ile Leu Thr Val Pro Ala Ala Met Thr
      20             25             30

```

```

Ser His Asp Leu Met Lys Phe Val Ala Pro Phe Asn Glu Val Ile Glu
      35             40             45

```

```

Gln Met Lys Ile Ile Arg Asp Ser Thr Pro Asn Gln Tyr Met Val Leu
      50             55             60

```

```

Ile Lys Phe Arg Ala Gln Ala Asp Ala Asp Ser Phe Tyr Met Thr Cys
      65             70             75             80

```

```

Asn Gly Arg Gln Phe Asn Ser Ile Glu Asp Asp Val Cys Gln Leu Val
      85             90             95

```

Tyr Val Glu Arg Ala Glu Val Leu Lys Ser Glu Asp Gly Ala Ser Leu  
 100 105 110  
 Pro Val Met Asp Leu Thr Glu Leu Pro Lys Cys Thr Val Cys Leu Glu  
 115 120 125  
 Arg Met Asp Glu Ser Val Asn Gly Ile Leu Thr Thr Leu Cys Asn His  
 130 135 140  
 Ser Phe His Ser Gln Cys Leu Gln Arg Trp Asp Asp Thr Thr Cys Pro  
 145 150 155 160  
 Val Cys Arg Tyr Cys Gln Thr Pro Glu Pro Val Glu Glu Asn Lys Cys  
 165 170 175  
 Phe Glu Cys Gly Val Gln Glu Asn Leu Trp Ile Cys Leu Ile Cys Gly  
 180 185 190  
 His Ile Gly Cys Gly Arg Tyr Val Ser Arg His Ala Tyr Lys His Phe  
 195 200 205  
 Glu Glu Thr Gln His Thr Tyr Ala Met Gln Leu Thr Asn His Arg Val  
 210 215 220  
 Trp Asp Tyr Ala Gly Asp Asn Tyr Val His Arg Leu Val Ala Ser Lys  
 225 230 235 240  
 Thr Asp Gly Lys Ile Val Gln Tyr Glu Cys Glu Gly Asp Thr Cys Gln  
 245 250 255  
 Glu Glu Lys Ile Asp Ala Leu Gln Leu Glu Tyr Ser Tyr Leu Leu Thr  
 260 265 270  
 Ser Gln Leu Glu Ser Gln Arg Ile Tyr Trp Glu Asn Lys Ile Val Arg  
 275 280 285  
 Ile Glu Lys Asp Thr Ala Glu Glu Ile Asn Asn Met Lys Thr Lys Phe  
 290 295 300  
 Lys Glu Thr Ile Glu Lys Cys Asp Asn Leu Glu His Lys Leu Asn Asp  
 305 310 315 320  
 Leu Leu Lys Glu Lys Gln Ser Val Glu Arg Lys Cys Thr Gln Leu Asn  
 325 330 335  
 Thr Lys Val Ala Lys Leu Lys Ser Gln Ser Gly Tyr Pro Ser Ile  
 340 345 350

&lt;210&gt; 27

&lt;211&gt; 460

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 27

cgagatgaag ccggcggtgg acgagatggt ccccgagggc gccgggccct acgtggacct 60  
 ggacgaggcg ggaggcagca ccgggctctt gatggacttg gcagccaatg aaaagccgtt 120  
 catgcagact tttttaacga ttttgaagat ctttttgatg atgatgacat ccagtgaatg 180  
 gccctctggc tgcaggcggg gcccaagccct tgggtacagag ccgcagtgtg agcctgcgca 240

ggacagtttc aggtgggtttt aaagaacacg tggaaatccc ttgaatttag gacctgggta 300  
 accagaaaga taagactggt cttaacgacc tagatgattc tgttcattctc tgaacgggat 360  
 caggttttgt cctcactcca attaaaagaa agcaatgtca catgaaaaaa aaaaaaaaaa 420  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 460

&lt;210&gt; 28

&lt;211&gt; 85

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 28

Met Lys Pro Ala Val Asp Glu Met Phe Pro Glu Gly Ala Gly Pro Tyr  
 1 5 10 15

Val Asp Leu Asp Glu Ala Gly Gly Ser Thr Gly Leu Leu Met Asp Leu  
 20 25 30

Ala Ala Asn Glu Lys Pro Phe Met Gln Thr Phe Leu Thr Ile Leu Lys  
 35 40 45

Ile Phe Leu Met Met Met Thr Ser Ser Glu Met Pro Ser Gly Cys Arg  
 50 55 60

Arg Gly Gln Ala Leu Gly Thr Glu Pro Gln Cys Glu Pro Ala Gln Asp  
 65 70 75 80

Ser Phe Arg Trp Phe  
 85

&lt;210&gt; 29

&lt;211&gt; 3204

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 29

gtttggcatc tgtggccgag ttgctgttgc cgggtgatag ttggagcgga gacttagcac 60  
 aatggcagaa cctgtttctc cactgaagca ctttgtgctg gctaagaagg cgattactgc 120  
 aatctttgac cagttactgg agttttgttac tgaaggatca cattttgttg aagcaacata 180  
 taagaatccg gaacttgatc gaatagccac tgaagatgat ctggtagaaa tgcaaggata 240  
 taaagacaag ctttccatca ttggtgaggt gctatctcgg agacacatga aggtggcatt 300  
 ttttggcagg acaagcagtg ggaagagctc tgttatcaat gcaatgttgt gggataaagt 360  
 tctccctagt gggattggcc atataaccaa ttgcttcccta agtgttgaag gaactgatgg 420  
 agataaaagg tatcttatga cagaaggatc agatgaaaaa aagagtgtga agacagttaa 480  
 tcaactggcc catgcccttc acatggacaa agatttgaaa gctggctgtc ttgtacgtgt 540  
 gttttggcca aaagcaaaat gtgccctctt gagagatgac ctgggtgttag tagacagtcc 600  
 aggcacagat gtcactacag agctggatag ctggattgat aagttttgcc tagatgctga 660  
 tgtctttgtt ttggtcgcaa actctgaatc aacactaatg aatacggaag aacacttttt 720  
 tcacaagggtg aatgagcggc tttccaagcc taatattttc attctcaata atcgttggga 780  
 tgcctctgca tcagagccag aatatatgga agcgtacgc agacagcaca tggaaagatg 840  
 cctgcatttc ttggtggagg agctcaaagt tgtaaatgct ttagaagcac agaatcgtat 900  
 cttctttgtt tcagcaaagg aagttcttag tgctagaaag caaaaagcac aggggatgcc 960  
 agaaagtggg gtggcacttg ctgaaggatt tcatgcaaga ttacaggaat ttcagaattt 1020  
 tgaacaaatc tttgaggagt gtatctcgca gtcagcagtg aaaacaaagt tcgaacagca 1080  
 cactatcaga gctaacaga tactagctac tgtgaaaaac ataattggatt cagtaaacct 1140  
 ggcagctgaa gataaaaggc attattcagt ggaagagagg gaagaccaaa ttgatagact 1200  
 ggactttatt cgaaaccaga tgaacctttt aacactggat gttaagaaaa aaatcaagga 1260  
 ggttaccgag gaggtggcaa acaaagtctt atgtgcaatg acagatgaaa tttgtcgact 1320  
 gtctgttttg gttgatgaat tttgttcaga gtttcatcct aatccagatg tattaataat 1380  
 atataaaagt gaattaaata agcacataga ggatgggatg ggaagaaatt tggctgatcg 1440



```

atgcaccgat gaagtaaacg ccttagtgcc tcagacccag caagaaatta ttgaaaattt 1500
gaagccatta cttccagctg gtatacagga taaactacat acactgatcc cttgcaagaa 1560
atttgatctc agttataatc taaattacca caagttatgt tcagattttc aagaggatat 1620
tgtatttcgt ttttccctgg gctggtcttc ccttgtagat cgatttttgg gccctagaaa 1680
tgctcaaagg gtgctcctag gattatcaga gcctatcttt cagctcccta gatcttttagc 1740
ttctactccc actgctccta cactccagc aacgccagat aatgcatcac aggaagaact 1800
catgattaca ttagtaacag gattggcgct cgttacatct agaacttcta tgggcatcat 1860
tattggttga ggagtgtatt ggaaaactat aggctggaaa ctctatctctg tttcattaac 1920
tatgtatgga gctttgtatc tttatgaaag actgagctgg accacccatg ccaaggagcg 1980
agccttttaa cagcagtttg taaactatgc aactgaaaaa ctgaggatga ttgttagctc 2040
cacgagtgc aactgcagtc accaagtaaa acaacaaata gctaccactt ttgctcgctc 2100
gtgccaaaca gttgatatta ctcaaaaaca gctggaagaa gaaattgcta gattacccaa 2160
agaaatagat cagttggaga aaatacaaaa caattcaaag ctcttaagaa ataaagctgt 2220
tcaacttgaa aatgagctgg agaattttac taagcagttt ctaccttcaa gcaatgaaga 2280
ctcctaacaa tagagattgc tttggtgacc atgataggag gaaacgaaac ttgtaagatt 2340
ggaacagttg ttatttttat gaaattactt taaatatgaa ttgtactaac tgtacctaaa 2400
tagcaaagcc ctgtgtatag tctggtaatg atctgtctca gggtagtgtt atttttgaag 2460
agtgttatgt ccttagtttt aattttgagt aaagaaaagg ctaaatcatg aattagttac 2520
aagcaacagt accaacttat gtgaccctg aggggtgggg ctgtgagctc ttaatttgtt 2580
tttgattctg aaaaactctg ctctctggca tccaggagtt agagattgag ctttcatct 2640
tctttctcaa aactagtttt tgatgctttc tttcatggga atagtcactt ttttatttag 2700
taaactcgat tgctggaacc accaaggagt gtggaatgtc cttgagtgtt ttatttatgc 2760
aagtcacagt cacgttgcca tcatggcagc tatgtgaaac actaataaat gtgtttttac 2820
tttttattcc cgttaaaact gatgtaaaac aggataaagg cttgttatag tcacttataa 2880
gtatctgggt ctaagtaatt tccttagatg tttctaaaga aacattttca gctttgctcc 2940
cattatgatt ccaataagga acgctttcct agtgcaattt taggagtaaa gtttgaagag 3000
ataaaaaatag ccaaagatag gagacgtctg aattttgaat gataaacagt gatgttttaa 3060
aaaagctgtt gttcttcagg aggcatttgc ctaggatatt gctggattat accccattgg 3120
aggcttttaa ttttatttgt atgaattttc caggatttca ttaaaaatta ttattgtatt 3180
ttttacctta aaaaaaaaaa aaaa

```

3204

&lt;210&gt; 30

&lt;211&gt; 741

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 30

```

Met Ala Glu Pro Val Ser Pro Leu Lys His Phe Val Leu Ala Lys Lys
  1             5             10             15

```

```

Ala Ile Thr Ala Ile Phe Asp Gln Leu Leu Glu Phe Val Thr Glu Gly
      20             25             30

```

```

Ser His Phe Val Glu Ala Thr Tyr Lys Asn Pro Glu Leu Asp Arg Ile
      35             40             45

```

```

Ala Thr Glu Asp Asp Leu Val Glu Met Gln Gly Tyr Lys Asp Lys Leu
      50             55             60

```

```

Ser Ile Ile Gly Glu Val Leu Ser Arg Arg His Met Lys Val Ala Phe
      65             70             75             80

```

```

Phe Gly Arg Thr Ser Ser Gly Lys Ser Ser Val Ile Asn Ala Met Leu
      85             90             95

```

```

Trp Asp Lys Val Leu Pro Ser Gly Ile Gly His Ile Thr Asn Cys Phe
      100            105            110

```

```

Leu Ser Val Glu Gly Thr Asp Gly Asp Lys Ala Tyr Leu Met Thr Glu
      115            120            125

```

Gly Ser Asp Glu Lys Lys Ser Val Lys Thr Val Asn Gln Leu Ala His  
 130 135 140  
 Ala Leu His Met Asp Lys Asp Leu Lys Ala Gly Cys Leu Val Arg Val  
 145 150 155 160  
 Phe Trp Pro Lys Ala Lys Cys Ala Leu Leu Arg Asp Asp Leu Val Leu  
 165 170 175  
 Val Asp Ser Pro Gly Thr Asp Val Thr Thr Glu Leu Asp Ser Trp Ile  
 180 185 190  
 Asp Lys Phe Cys Leu Asp Ala Asp Val Phe Val Leu Val Ala Asn Ser  
 195 200 205  
 Glu Ser Thr Leu Met Asn Thr Glu Lys His Phe Phe His Lys Val Asn  
 210 215 220  
 Glu Arg Leu Ser Lys Pro Asn Ile Phe Ile Leu Asn Asn Arg Trp Asp  
 225 230 235 240  
 Ala Ser Ala Ser Glu Pro Glu Tyr Met Glu Asp Val Arg Arg Gln His  
 245 250 255  
 Met Glu Arg Cys Leu His Phe Leu Val Glu Glu Leu Lys Val Val Asn  
 260 265 270  
 Ala Leu Glu Ala Gln Asn Arg Ile Phe Phe Val Ser Ala Lys Glu Val  
 275 280 285  
 Leu Ser Ala Arg Lys Gln Lys Ala Gln Gly Met Pro Glu Ser Gly Val  
 290 295 300  
 Ala Leu Ala Glu Gly Phe His Ala Arg Leu Gln Glu Phe Gln Asn Phe  
 305 310 315 320  
 Glu Gln Ile Phe Glu Glu Cys Ile Ser Gln Ser Ala Val Lys Thr Lys  
 325 330 335  
 Phe Glu Gln His Thr Ile Arg Ala Lys Gln Ile Leu Ala Thr Val Lys  
 340 345 350  
 Asn Ile Met Asp Ser Val Asn Leu Ala Ala Glu Asp Lys Arg His Tyr  
 355 360 365  
 Ser Val Glu Glu Arg Glu Asp Gln Ile Asp Arg Leu Asp Phe Ile Arg  
 370 375 380  
 Asn Gln Met Asn Leu Leu Thr Leu Asp Val Lys Lys Lys Ile Lys Glu  
 385 390 395 400  
 Val Thr Glu Glu Val Ala Asn Lys Val Ser Cys Ala Met Thr Asp Glu  
 405 410 415  
 Ile Cys Arg Leu Ser Val Leu Val Asp Glu Phe Cys Ser Glu Phe His  
 420 425 430  
 Pro Asn Pro Asp Val Leu Lys Ile Tyr Lys Ser Glu Leu Asn Lys His  
 435 440 445

Ile Glu Asp Gly Met Gly Arg Asn Leu Ala Asp Arg Cys Thr Asp Glu  
 450 455 460  
 Val Asn Ala Leu Val Pro Gln Thr Gln Gln Glu Ile Ile Glu Asn Leu  
 465 470 475 480  
 Lys Pro Leu Leu Pro Ala Gly Ile Gln Asp Lys Leu His Thr Leu Ile  
 485 490 495  
 Pro Cys Lys Lys Phe Asp Leu Ser Tyr Asn Leu Asn Tyr His Lys Leu  
 500 505 510  
 Cys Ser Asp Phe Gln Glu Asp Ile Val Phe Arg Phe Ser Leu Gly Trp  
 515 520 525  
 Ser Ser Leu Val His Arg Phe Leu Gly Pro Arg Asn Ala Gln Arg Val  
 530 535 540  
 Leu Leu Gly Leu Ser Glu Pro Ile Phe Gln Leu Pro Arg Ser Leu Ala  
 545 550 555 560  
 Ser Thr Pro Thr Ala Pro Thr Thr Pro Ala Thr Pro Asp Asn Ala Ser  
 565 570 575  
 Gln Glu Glu Leu Met Ile Thr Leu Val Thr Gly Leu Ala Ser Val Thr  
 580 585 590  
 Ser Arg Thr Ser Met Gly Ile Ile Ile Val Gly Gly Val Ile Trp Lys  
 595 600 605  
 Thr Ile Gly Trp Lys Leu Leu Ser Val Ser Leu Thr Met Tyr Gly Ala  
 610 615 620  
 Leu Tyr Leu Tyr Glu Arg Leu Ser Trp Thr Thr His Ala Lys Glu Arg  
 625 630 635 640  
 Ala Phe Lys Gln Gln Phe Val Asn Tyr Ala Thr Glu Lys Leu Arg Met  
 645 650 655  
 Ile Val Ser Ser Thr Ser Ala Asn Cys Ser His Gln Val Lys Gln Gln  
 660 665 670  
 Ile Ala Thr Thr Phe Ala Arg Leu Cys Gln Gln Val Asp Ile Thr Gln  
 675 680 685  
 Lys Gln Leu Glu Glu Glu Ile Ala Arg Leu Pro Lys Glu Ile Asp Gln  
 690 695 700  
 Leu Glu Lys Ile Gln Asn Asn Ser Lys Leu Leu Arg Asn Lys Ala Val  
 705 710 715 720  
 Gln Leu Glu Asn Glu Leu Glu Asn Phe Thr Lys Gln Phe Leu Pro Ser  
 725 730 735  
 Ser Asn Glu Asp Ser  
 740

&lt;210&gt; 31

&lt;211&gt; 2483

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 31

```

cacatgttgc cccaaataca agcacaaatc taaccatgag cttcagcaat cagctcaata 60
cagtgcacaa tcaggccagt gttctagctt ccagttctac tgcagcagct gctactcttt 120
ctctggctaa ttcagatgtc tcactactaa actaccagtc agctttgtac ccatcatctg 180
ctgcaccagt tcctggagtt gcccagcagg gtgtttcctt gcagcctgga accacccaga 240
tttgactca gacagatcca ttccaacaga catttatagt atgtccacct gcgtttcaaa 300
ctggactaca agcaacaaca aagcattctg gattccctgt gaggatggat aatgctgtac 360
cgattgtacc ccaggcacca gctgctcagc ccactacaga ttcagtcagg agttctcacg 420
cagacttgca gggaaaaaat atccagacat tcttgagaaa tggctctctg aggaagctgt 480
acaccactaa tggtagcaac tctccacct caagtagcca catcacaccg cagtatgcgg 540
tgccctttac tctgagctgc gcagccggcc ggccggcgct ggttgaacag actgccgctg 600
tactgcaggc gtggcctgga gggactcagc aaattctcct gccttcaact tggcaacagt 660
tgcctggggt agctctacac aactctgtcc agcccacagc aatgattcca gaggccatgg 720
ggagtggaca gcagctagct gactggagga atgcccactc tcatggcaac cagtacagca 780
ctatcatgca gcagccatcc ttgctgacta accatgtgac attggccact gctcagcctc 840
tgaatgttgg tgttgcccat gttgtcagac aacaacaatc cagttccctc ccttcgaaga 900
agaataagca gtcagctcca gtctcttcca agtctctctc agatgttctg ccttcccaag 960
tctattctct ggttgggagc agtcccctcc gcaccacatc ttcttataat tccttgggtc 1020
ctgtccaaga tcagcatcag cccatcatca ttccagatac tcccagccct cctgtgagtg 1080
tcatcactat ccgaagtgc actgatgagg aagaggacaa caaatacaag ccagtagct 1140
ctggactgaa gccaaagtct aatgtcatca gttatgtcac tgtcaatgat tctccagact 1200
ctgactcttc tttgagcagc ccttattcca ctgataccct gagtgtcttc cgaggcaata 1260
gtggatccgt tttggagggg cctggcagag ttgtggcaga tggcactggc acccgacta 1320
tcattgtgcc tccactgaaa actcagcttg gtgactgcac tgtagcaacc caggcctcag 1380
gtctcctgag caataagact aagccagtcg cttcagtgag tgggcagtc tctggatgct 1440
gtatcacccc cacagggtat cgagctcaac gcggggggac cagtgcagca caaccactca 1500
atcttagcca gaaccagcag tcatcgcgcg ctccaacctc acaggagaga agcagcaacc 1560
cagccccccg caggcagcag gcgtttgtgg cccctctctc ccaagcccc tacaccttc 1620
agcatggcag cccgctacac tcgacagggc acccacacct tgccccggcc cctgctcacc 1680
tgccaagcca ggctcatctg tatacgtatg ctgccccgac ttctgctgct gcactgggct 1740
caaccagctc cattgctcat cttttctccc cacagggttc ctcaaggcat gctgcagcct 1800
ataccactca ccttagcact ttggtgcacc aggtccctgt cagtgttggg cccagcctcc 1860
tcacttctgc cagcgtggcc cctgctcagt accaacacca gtttgccacc caatcctaca 1920
ttgggtcttc ccgaggctca acaatttaca ctggataccc gctgagtcct accaagatca 1980
gccagtattc ctacttatag ttggtgagca tgagggagga ggaatcatgg ctaccttctc 2040
ctggccctgc gttcttaata ttgggctatg gagagatcct cctttaccct cttgaaattt 2100
cttagccagc aacttgttct gcagggggccc actgaagcag aagggttttc tctgggggaa 2160
cctgtctcag tgttgactgc attgtttag tcttcccaa gtttgcccta tttttaaat 2220
cattattttt gtgacagtaa ttttggtag ttggaagagt cagatgcca tcttctgcag 2280
ttaccaagga agagagattg ttctgaagtt accctctgaa aaatattttg tctctctgac 2340
ttgatttcta taaatgcttt taaaaacaag tgaagcccct ctttatttca ttttgtgta 2400
ttgtgattgc tggtcaggaa aaatgctgat agaaggagt gaaatctgat gacaaaaaaa 2460
aaaaaaaaa aaaaaaaaaa aaa

```

2483

&lt;210&gt; 32

&lt;211&gt; 654

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 32

```

Met Ser Phe Ser Asn Gln Leu Asn Thr Val His Asn Gln Ala Ser Val
  1             5             10             15
Leu Ala Ser Ser Ser Thr Ala Ala Ala Thr Leu Ser Leu Ala Asn
          20             25             30

```

Ser Asp Val Ser Leu Leu Asn Tyr Gln Ser Ala Leu Tyr Pro Ser Ser  
 35 40 45  
 Ala Ala Pro Val Pro Gly Val Ala Gln Gln Gly Val Ser Leu Gln Pro  
 50 55 60  
 Gly Thr Thr Gln Ile Cys Thr Gln Thr Asp Pro Phe Gln Gln Thr Phe  
 65 70 75 80  
 Ile Val Cys Pro Pro Ala Phe Gln Thr Gly Leu Gln Ala Thr Thr Lys  
 85 90 95  
 His Ser Gly Phe Pro Val Arg Met Asp Asn Ala Val Pro Ile Val Pro  
 100 105 110  
 Gln Ala Pro Ala Ala Gln Pro Thr Thr Asp Ser Val Arg Ser Ser His  
 115 120 125  
 Ala Asp Leu Gln Gly Lys Asn Ile Gln Thr Phe Leu Arg Asn Gly Leu  
 130 135 140  
 Leu Arg Lys Leu Tyr Thr Thr Asn Gly Ser Asn Ser Pro Pro Ser Ser  
 145 150 155 160  
 Ser His Ile Thr Pro Gln Tyr Ala Val Pro Phe Thr Leu Ser Cys Ala  
 165 170 175  
 Ala Gly Arg Pro Ala Leu Val Glu Gln Thr Ala Ala Val Leu Gln Ala  
 180 185 190  
 Trp Pro Gly Gly Thr Gln Gln Ile Leu Leu Pro Ser Thr Trp Gln Gln  
 195 200 205  
 Leu Pro Gly Val Ala Leu His Asn Ser Val Gln Pro Thr Ala Met Ile  
 210 215 220  
 Pro Glu Ala Met Gly Ser Gly Gln Gln Leu Ala Asp Trp Arg Asn Ala  
 225 230 235 240  
 His Ser His Gly Asn Gln Tyr Ser Thr Ile Met Gln Gln Pro Ser Leu  
 245 250 255  
 Leu Thr Asn His Val Thr Leu Ala Thr Ala Gln Pro Leu Asn Val Gly  
 260 265 270  
 Val Ala His Val Val Arg Gln Gln Gln Ser Ser Ser Leu Pro Ser Lys  
 275 280 285  
 Lys Asn Lys Gln Ser Ala Pro Val Ser Ser Lys Ser Ser Leu Asp Val  
 290 295 300  
 Leu Pro Ser Gln Val Tyr Ser Leu Val Gly Ser Ser Pro Leu Arg Thr  
 305 310 315 320  
 Thr Ser Ser Tyr Asn Ser Leu Val Pro Val Gln Asp Gln His Gln Pro  
 325 330 335  
 Ile Ile Ile Pro Asp Thr Pro Ser Pro Pro Val Ser Val Ile Thr Ile  
 340 345 350

Arg Ser Asp Thr Asp Glu Glu Glu Asp Asn Lys Tyr Lys Pro Ser Ser  
 355 360 365  
 Ser Gly Leu Lys Pro Arg Ser Asn Val Ile Ser Tyr Val Thr Val Asn  
 370 375 380  
 Asp Ser Pro Asp Ser Asp Ser Ser Leu Ser Ser Pro Tyr Ser Thr Asp  
 385 390 395 400  
 Thr Leu Ser Ala Leu Arg Gly Asn Ser Gly Ser Val Leu Glu Gly Pro  
 405 410 415  
 Gly Arg Val Val Ala Asp Gly Thr Gly Thr Arg Thr Ile Ile Val Pro  
 420 425 430  
 Pro Leu Lys Thr Gln Leu Gly Asp Cys Thr Val Ala Thr Gln Ala Ser  
 435 440 445  
 Gly Leu Leu Ser Asn Lys Thr Lys Pro Val Ala Ser Val Ser Gly Gln  
 450 455 460  
 Ser Ser Gly Cys Cys Ile Thr Pro Thr Gly Tyr Arg Ala Gln Arg Gly  
 465 470 475 480  
 Gly Thr Ser Ala Ala Gln Pro Leu Asn Leu Ser Gln Asn Gln Gln Ser  
 485 490 495  
 Ser Ala Ala Pro Thr Ser Gln Glu Arg Ser Ser Asn Pro Ala Pro Arg  
 500 505 510  
 Arg Gln Gln Ala Phe Val Ala Pro Leu Ser Gln Ala Pro Tyr Thr Phe  
 515 520 525  
 Gln His Gly Ser Pro Leu His Ser Thr Gly His Pro His Leu Ala Pro  
 530 535 540  
 Ala Pro Ala His Leu Pro Ser Gln Ala His Leu Tyr Thr Tyr Ala Ala  
 545 550 555 560  
 Pro Thr Ser Ala Ala Ala Leu Gly Ser Thr Ser Ser Ile Ala His Leu  
 565 570 575  
 Phe Ser Pro Gln Gly Ser Ser Arg His Ala Ala Ala Tyr Thr Thr His  
 580 585 590  
 Pro Ser Thr Leu Val His Gln Val Pro Val Ser Val Gly Pro Ser Leu  
 595 600 605  
 Leu Thr Ser Ala Ser Val Ala Pro Ala Gln Tyr Gln His Gln Phe Ala  
 610 615 620  
 Thr Gln Ser Tyr Ile Gly Ser Ser Arg Gly Ser Thr Ile Tyr Thr Gly  
 625 630 635 640  
 Tyr Pro Leu Ser Pro Thr Lys Ile Ser Gln Tyr Ser Tyr Leu  
 645 650

&lt;210&gt; 33

&lt;211&gt; 2731

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (2173)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (2700)

&lt;400&gt; 33

```
ggcactccac ggctgtgaag atggcggcgg ctgctgtggt tcaggtgttg cctgtcattc 60
ttctgtctct gggagctcac ccgtcaccac tgtcgttttt cagtgcggga ccggcaaccg 120
tagctgctgc cgaccggtcc aaatggcaca ttccgatacc gtcggggaaa aattatttta 180
gttttggaag gatcctcttc agaaatacca ctatcttctt gaagtttgat ggagaacctt 240
gtgacctgtc tttgaatata acctggtatc tgaagagcgc tgattgttac aatgaaatct 300
ataacttcaa ggcagaagaa gtagagttgt atttggaata acttaaggaa aaaagaggct 360
tgtctgggaa atatcaaaca tcatcaaaat tgttccagaa ctgcagttaa ctctttaaaa 420
cacagacctt ttctggagat tttatgcata gactgcctct tttaggagaa aaacaggagg 480
ctaaggagaa tggacaacaa cttaccttta ttggagacaa aaccgcaatg catgaacct 540
tgcaaacctg gcaagatgca ccatacattt ttattgtaca tattggcatt tcatcctcaa 600
aggaatcatc aaaagaaaat tctactgagta atctttttac catgactgtt gaagtgaagg 660
gtccctatga atacctcaca cttgaagact atcccttgat gatttttttc atggtgatgt 720
gtattgtata tgtcctgttt ggtgttctgt ggctggcatg gtctgcctgc tactggagag 780
atctcctgag aattcagttt tggattggtg ctgtcatctt cctgggaatg cttgagaaag 840
ctgtcttcta tgcggaattt cagaatatcc gacacaaagg agaactctgc caggggtgctt 900
tgatccttgc agagctgctt tcagcagtga aacgctcact ggctcgaacc ctggtcatca 960
tagtcagctc gggatatggc atcgtcaagc cagccttggt agtcactctt cataagggtt 1020
tagtagcagg agccctctat ctttgttctt ctggcatgga aggggtcctc agagttactg 1080
gggcccagac tgatcttgct tccttggcct ttatccctt ggctttccta gacactgcct 1140
tgtgtgtgtg gatatttatt agcctgactc aaacaatgaa gctattaaaa cttcggagga 1200
acattgtaaa actctctttg tatcggcatt tcaccaacac gcttattttg gcagtggcag 1260
catccattgt gtttatcatc tggacaacca tgaagttcag aatagtgaac tgctagtcgg 1320
tgagttataa gcacatttat gaataatgta ctgtcttata aacaactgat ggtgttgatg 1380
acagtggtaa ggttcttcta agttatatac cttataaaaa attagagcta ggtctctact 1440
ctgagggttg tgatacttcc ctccctctaa gtattctgta ctatcatggt gcttgggtata 1500
gtactttttt gtttgttttt tctgactgta ttctccctgt tttgggagag aattttgtta 1560
gttataacta cagtgtgcta taaccagtc ttattttaac taaaaatctt aagaagtcca 1620
gagtactaaa tattaagtac catatgtgta aataatacta atctgaatag aagccacatc 1680
cttaagatct gagctcaacg actgtgacag taggatttct tcagaagcag ctaaggctct 1740
tattttgttc aataaataat gaaaatgaaa attataaagt ataccaacct aatgtaacct 1800
tctcttacac tgtataaggt aactttctct taaccctgta taaaaccctt tcttaaagct 1860
tctcagaggg atgatgaagc ttgacaaat actctgttcc gttgatgcat tttctttaac 1920
aacagtaagc actacaaggg caaaaactac attcattcac tttgtttccc cacacttacc 1980
acagtactga gcacgtagca ggctcttagt aaacataact tgaatgaaca aataagtgat 2040
ttttgttgta tgccaaaggg tttatgaaca aggggttaag ataagtgtga tgaatgttgt 2100
acttctcccc tgtattgtag gactggcggg agctgtgggt agacgatgcc atctggcgct 2160
tgctgttctc cangatctct tttgtcatca tgggtctctg gcgaccatct gcaacaacc 2220
agaggttctt ggactcttct gtttactctg ctaacatgag atgaccatgt catcaattag 2280
gggtggtgca ttgggggaca gtatcagggc tgtgtcatat agtgaagga acactgggcc 2340
tggaatcaga agaactgggt tcctatctca gctctctct taacttcatg atttttgcca 2400
tgcgccctct ccacctctct ggccttagtt tcctttctat atactgaggg ggaattaaac 2460
ccagcaacat gaagttcctt tcagctctga cattttgtga taaatacaca ggcatactat 2520
ggaaataaat tgcaagtttg gtttcagacc atcacgataa agcagatatt gagttacata 2580
catattttgt ttttccagt gcatatcaaa gttatgttta cactattctg tagtctacta 2640
tgtgtgcaat agcattatgt ctaaaaaata tatgcaggtt aatttaaaaa cactttgttn 2700
ccaaaaaaaa aaaaaaaaaa aaaaaaaaaa a
```

2731

&lt;210&gt; 34

<211> 441  
 <212> PRT  
 <213> Homo sapiens

<400> 34

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu  
 1 5 10 15

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala  
 20 25 30

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser  
 35 40 45

Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr  
 50 55 60

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile  
 65 70 75 80

Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe  
 85 90 95

Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg  
 100 105 110

Gly Leu Ser Gly Lys Tyr Gln Thr Ser Ser Lys Leu Phe Gln Asn Cys  
 115 120 125

Ser Glu Leu Phe Lys Thr Gln Thr Phe Ser Gly Asp Phe Met His Arg  
 130 135 140

Leu Pro Leu Leu Gly Glu Lys Gln Glu Ala Lys Glu Asn Gly Thr Asn  
 145 150 155 160

Leu Thr Phe Ile Gly Asp Lys Thr Ala Met His Glu Pro Leu Gln Thr  
 165 170 175

Trp Gln Asp Ala Pro Tyr Ile Phe Ile Val His Ile Gly Ile Ser Ser  
 180 185 190

Ser Lys Glu Ser Ser Lys Glu Asn Ser Leu Ser Asn Leu Phe Thr Met  
 195 200 205

Thr Val Glu Val Lys Gly Pro Tyr Glu Tyr Leu Thr Leu Glu Asp Tyr  
 210 215 220

Pro Leu Met Ile Phe Phe Met Val Met Cys Ile Val Tyr Val Leu Phe  
 225 230 235 240

Gly Val Leu Trp Leu Ala Trp Ser Ala Cys Tyr Trp Arg Asp Leu Leu  
 245 250 255

Arg Ile Gln Phe Trp Ile Gly Ala Val Ile Phe Leu Gly Met Leu Glu  
 260 265 270

Lys Ala Val Phe Tyr Ala Glu Phe Gln Asn Ile Arg His Lys Gly Glu  
 275 280 285

Ser Val Gln Gly Ala Leu Ile Leu Ala Glu Leu Leu Ser Ala Val Lys



290 295 300  
 Arg Ser Leu Ala Arg Thr Leu Val Ile Ile Val Ser Leu Gly Tyr Gly  
 305 310 315 320  
 Ile Val Lys Pro Arg Leu Gly Val Thr Leu His Lys Val Val Val Ala  
 325 330 335  
 Gly Ala Leu Tyr Leu Leu Phe Ser Gly Met Glu Gly Val Leu Arg Val  
 340 345 350  
 Thr Gly Ala Gln Thr Asp Leu Ala Ser Leu Ala Phe Ile Pro Leu Ala  
 355 360 365  
 Phe Leu Asp Thr Ala Leu Cys Trp Trp Ile Phe Ile Ser Leu Thr Gln  
 370 375 380  
 Thr Met Lys Leu Leu Lys Leu Arg Arg Asn Ile Val Lys Leu Ser Leu  
 385 390 395 400  
 Tyr Arg His Phe Thr Asn Thr Leu Ile Leu Ala Val Ala Ala Ser Ile  
 405 410 415  
 Val Phe Ile Ile Trp Thr Thr Met Lys Phe Arg Ile Val Thr Cys Gln  
 420 425 430  
 Ser Val Ser Tyr Lys His Ile Tyr Glu  
 435 440

&lt;210&gt; 35

&lt;211&gt; 1670

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 35

aatcgggctc accccaagt tggggcgggtc attgacaagt cgaagagttg ggtccttggtg 60  
 tatgcatggg tgggatggta agggagaag ccctggcctg gatgtgccgg gaaccccggga 120  
 aagccttctc agccattggt gggcctagcc tgggaccgga cagcactcct ggggtggggga 180  
 ctggggagtg ggcaacaggt ggagccatcc ttggcagacc gaccccatgt gcagtccttg 240  
 ggacaggttt ctccctcctg agcaattgta gctccctcctg agggccagtt ccagagacag 300  
 gccgagggtg gcgagtcctc accccatgct ctcttccaga cctcctacga gatgatgatg 360  
 cagtgtgtgt cccgcatggt ggcccacccc ctgcatgtca tctcaatgcg ctgcatggtc 420  
 cagtttgtgg gacgggaggg caagtacagt ggtgtgctga gctccattgg gaagattttc 480  
 aaagaggaag ggctgctggg attcttcgtt ggattaatcc ctcacctcct gggcgatgtg 540  
 gttttcttgt ggggctgtaa cctgctggcc cacttcatca atgcctacct ggtggatgac 600  
 agcttcagcc aggcctggc catccggagc tataccaagt tcgtgatggg gattgcagtg 660  
 agcatgtga cctacccctt cctgctagt ttggcagctca tggctgtgaa caactgcggg 720  
 ctgcaagctg ggctccccc ttactcccca gtgttcaa cctggattca ctgctggaag 780  
 tacctgagtg tgcagggcca gctcttccga ggctccagcc tgcttttccg ccgggtgtca 840  
 tcaggatcat gctttgccct ggagtaacct gaatcatcta aaaaacacgg tctcaacctg 900  
 gccaccgtgg gtgaggcctg accaccttgg gacacctgca agacgactcc aacccaacaa 960  
 caaccagatg tgctccagcc cagccgggct tcagttccat atttgccatg tgtctgtcca 1020  
 gatgtggggg tgagcggggg tggggctgca cccagtggat tgggtcaccc ggcagaccta 1080  
 gggaaggtga ggcgaggtgg ggagttggca gaatcccat acctcgcaga tttgctgagt 1140  
 ctgtcttgtg cagagggcca gagaatggct tatgggggcc caggttggat ggggaaaggc 1200  
 taatgggggc agaccccacc ccgtctaccc ctccagtcag ccagcgcgcc atcctgcagc 1260  
 tcagctggga gcatcattct cctgcttgt acataggggtg tgggtcccctg gcacgtggcc 1320  
 accatcatgt ctaggcctat gctaggaggc aaatggccag gctctgcctg tgtttttctc 1380  
 aacactactt ttctgatatg agggcagcac ctgcctctga atgggaaatc atgcaactac 1440

tcagaatgtg tcctcctcat ctaatgetca tctgtttaat ggtgatgcct cgcgtacagg 1500  
 atctgggttac ctgtgcagtt gtgaataccc agaggttggg cagatcagtg tctctagtc 1560  
 taccagttt taaagttcat ggtaagattt gacctcatct cccgcaaata aatgtattgg 1620  
 tgatttggaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1670

<210> 36  
 <211> 164  
 <212> PRT  
 <213> Homo sapiens

<400> 36  
 Met Gly Gly Met Val Arg Glu Glu Ala Leu Ala Trp Met Cys Arg Glu  
 1 5 10 15  
 Pro Arg Lys Ala Phe Ser Ala Ile Val Gly Pro Ser Leu Gly Pro Asp  
 20 25 30  
 Ser Thr Pro Gly Trp Gly Thr Gly Glu Trp Ala Thr Gly Gly Ala Ile  
 35 40 45  
 Leu Gly Arg Pro Thr Pro Cys Ala Val Pro Gly Thr Gly Phe Ser Leu  
 50 55 60  
 Leu Ser Thr Cys Ser Ser Pro Arg Gly Pro Val Pro Glu Thr Gly Arg  
 65 70 75 80  
 Gly Trp Arg Val Pro Thr Pro Cys Ser Leu Pro Asp Leu Leu Arg Asp  
 85 90 95  
 Asp Asp Ala Val Cys Val Pro His Val Gly Pro Pro Pro Ala Cys His  
 100 105 110  
 Leu Asn Ala Leu His Gly Pro Val Cys Gly Thr Gly Gly Gln Val Gln  
 115 120 125  
 Trp Cys Ala Glu Leu His Trp Glu Asp Phe Gln Arg Gly Arg Ala Ala  
 130 135 140  
 Gly Ile Leu Arg Trp Ile Asn Pro Ser Pro Pro Gly Arg Cys Gly Phe  
 145 150 155 160  
 Leu Val Gly Leu

<210> 37  
 <211> 1493  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (1415)

<400> 37  
 ggatggcgcg cgcggggccc gcacgtggag gccggcgcg gggcgcgggc agggccggct 60  
 gctgagacgc gctgctgccc cccgcgcggg cgccgcggct tcaatggcgc catcgcccag 120  
 gaccggcagc cggcaagatg cgaccgccct gccagcatg tcctcaactt tctgggcgtt 180  
 catgatcctg gccagcctgc tcatgccta ctgcagtcag ctggcgccgc gcacctgtga 240  
 gattgtgacc ttggaccggg acagcagcca gcctcggagg acgatcgccc ggcagaccgc 300

```

ccgctgtgcg tgtagaaagg ggcagatcgc cggcaccacg agagcccggc cgcctgtgt 360
ggacgcaaga atcatcaaga ccaagcagtg gtgtgacatg cttccgtgtc tggaggggga 420
aggctgcgac ttgttaatca accggtcagg ctggacgtgc acgcagcccg gcgggaggat 480
aaagaccacc acggtctcct gacaaacaca gcccctgagg gggcccggga gtggccttgg 540
ctccctggag agcccacgtc tcagccacag ttctccactc gcctcggact tcaaccgttc 600
tctgccgccc gcccactccg tttccctgtg gtccgtgaag gacggcctca ggccttggca 660
tcctgagctt ctgtctgtcc agccgacccg aggaggcccg actcagacac ataggcgggg 720
ggcggcacct ggcacagca atacgcagtc tgtgggagcc cggccgcgcc cagccccgc 780
cgaccgtggc gttggccctg ctgtcctcag aggaggagga ggaggaggca gctccggcag 840
ccacagaagg ctgcagccca gcccgcctga gacacgacgc ctgcccaggg ggactgtcag 900
gcacagaagc ggctcctccc cgtgccccag actgtccgaa ttggttttat tttcttatac 960
tttcagtata ctccatagac caaagagcaa aatctatctg aacctggacg caccctcact 1020
gtcaggggtcc ctgggggtcg ttgtgcgggc gggagggcaa tgggtggcaga gacatgtgt 1080
ggccccggcg gacgagagag ggcggccgtg gtggaggcct ccaccccagg agcaccgccg 1140
gcaccctcgg aggacgggtt tcggctgcgc ggaggccgtg gcacacctgc gggaggcagc 1200
gacggccccc acgcagacgc cgggaacgca ggccgcttta ttcctctgta cttagatcaa 1260
cttgaccgta ctaaaatccc tttctgtttt aaccagttaa acatgcctct tctacagtc 1320
catttttgat agttggataa tccagtatct gccaagagca tgttgggtct cccgtgactg 1380
ctgcctcatc gataccat ttagctccag aaagnaaaga aaactcgagt aacacttgtt 1440
tgaaagagat cattaatgt attttgcaaa gcctaaaaaa aaaaaaaaaa aaa 1493

```

&lt;210&gt; 38

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

```

Met Ala Pro Ser Pro Arg Thr Gly Ser Arg Gln Asp Ala Thr Ala Leu
  1                      5                      10                      15

Pro Ser Met Ser Ser Thr Phe Trp Ala Phe Met Ile Leu Ala Ser Leu
          20                      25                      30

Leu Ile Ala Tyr Cys Ser Gln Leu Ala Ala Gly Thr Cys Glu Ile Val
      35                      40                      45

Thr Leu Asp Arg Asp Ser Ser Gln Pro Arg Arg Thr Ile Ala Arg Gln
  50                      55                      60

Thr Ala Arg Cys Ala Cys Arg Lys Gly Gln Ile Ala Gly Thr Thr Arg
  65                      70                      75                      80

Ala Arg Pro Ala Cys Val Asp Ala Arg Ile Ile Lys Thr Lys Gln Trp
          85                      90                      95

Cys Asp Met Leu Pro Cys Leu Glu Gly Glu Gly Cys Asp Leu Leu Ile
      100                      105                      110

Asn Arg Ser Gly Trp Thr Cys Thr Gln Pro Gly Gly Arg Ile Lys Thr
      115                      120                      125

Thr Thr Val Ser
      130

```

&lt;210&gt; 39

&lt;211&gt; 3693

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (108)

&lt;400&gt; 39

```

cgtggccgaa ggatgcccgt ttgtgtctaa acggaggctc ggccacaacg cccctggatt 60
ggtggtaggg cggggcgggc cacagtctcc accctgaagc ggaagtgnag gaaagatgga 120
ggaccatcac cacgtgccca tcgacatcca gaccagccag ctgctcgatt ggctggtgga 180
cagaaggcac tgcagcctga aatggcagag tctggtgctg acgatccgag agaagatcaa 240
tgctgccatc caggacatgc cagagagcga agagatcgcc cagctgctgt ctgggtcctg 300
tgagtgtcta ggggctgtca ctggagtccc ctctttgctg aggtagtatg tatcagctga 360
gctactctct tgttatttag ccaccagggc tggcctttag agagggagcg atttttatatt 420
gaggtataga tctggcttc ttccactatg aaatgattta gggaaaagct acacactaaa 480
gttactggca gtatattata catgaatcag ccacctgcag tgcccagagt aggtgaagaa 540
gatacttttag ttctcgaaat cccgtctctt gctttctaga cattcactac tttcactgcc 600
taagaatcct ggacctcttc aaaggcacag aggcctccac gaagaatatt tttggccgat 660
actcttcaca gcggatgaag gattggcagg agattatagc tctgtatgag aaggacaaca 720
cctacttagg taaagtggcc cggcctggga gccctggtat ccatggggaa gccactctc 780
agagtcttga gataccaggc ttataggagg cacagtctgt gagtgggaag agactggagt 840
gtagatgttg cccatttcta ggtggtaaaa tcaattgttt ttgatggaat tgattttccc 900
tgagtggagt gctgggggaa ggaggaggct caggccggtg gtggccattc gccgtgcctc 960
agcgagcagg tgtgtgtggg tcctccacca ctacacctct ggtagcggg agtgtgtctg 1020
ccccaccccc acccccgtag cccattgta cacaaggcag aagaggcacg ggttttctctg 1080
ggagcgaata tcaagtgcct gagagcaact caggactaa ctgtgttttg gttgggtgta 1140
gtataaataa taataatggc taatatcttc tgagcatcta ctaaatgcaa ggaattgtgc 1200
ttggtgtgtc atgtggattc tctcttgcat ctctcatgata aatgttattg tcgctgtttt 1260
accgatgagg gttggattag aggggttaaa caacttgtct taggctccac agctgggaac 1320
aagtggggct gggaagctga ctctgtgtc ttcaccacca caaaggatgt gtgtgcatcc 1380
tggggcatgc ctgcctcatg tgggggtgtc ctgggctgaa tttcctgggc actctcagt 1440
ggaactctct agcctcctgg ttcggaatgt caactatgag atccctcacc tgaagaagca 1500
gattgccaaag tgccagcagc tgcagcaaga atacagccgc aaggaggagg agtgccaggc 1560
aggggctgcc gagatcgagg agcagttcta cactcctgc aagcagtatg gcatacaggt 1620
gagcggcggc agcctctctg cagccagagg acacctgggc cctgcttgt ctctcttga 1680
ccccgtctga cccctcagcc tgggtgcgcc cctttggggc cagtgtctta cttttctctg 1740
gtctttggat gttttcttca atctgttgga ctccacctct tctccctct ctaggcgcaa 1800
aatgtccgag gagaactgct ggccctggtg aaggacctgc cgagtcagct ggctgagatt 1860
ggggcagcgg ctacagcagc cctgggggaa gccattgacg tgtaccaggc gtctgtgggg 1920
tttgtgtgtg agaggttagg aggcctcagc ttctcctggt gggggtgctt tgcctgtgtt 1980
ccccagctca tgacccttct ccagtgtct tgttcccata taacatttga actctttaca 2040
cacctgaacc tgtggggggc ttgcccattt gacctgtgg cccaggccaa agcccagtg 2100
tggccttacg catggtcggc aggagagtca gttgtgtgct ctgttgaaag ccacagagc 2160
aggtgttgcc aatgtgcggg ttcgtgcaga agcggggaaa ctcaacggtg tacgagtgga 2220
ggacagggac agagccctct gtggtggaac gacccacct cgaggagctt cctgagcagg 2280
tggcagaaga tgcgattgac tggggcgact ttggggtaga ggcagtgtct gaggggactg 2340
actctggcat ctctgccgag gctgctggaa tgcactgggg catcttccc gaatcagatt 2400
caaaggatcc tggaggatg gggatagact ggggagacga tgctgttgct ttgcagatca 2460
cagtgtgga agcaggaacc caggctccag aaggtgttgc caggggcccc gatgccctga 2520
cactgcttga atacactgag acccggaatc agttccttga tgagctcatg gagcttgaga 2580
tcttcttagc ccagagagca gtggagtga gtgaggaggc agatgtcctg tctgtgagcc 2640
agttccagct ggctccagcc atcctgcagg gccagaccaa agagaagatg gttaccatgg 2700
tgtcagtgct ggaggatctg attggcaagc ttaccagtct tcagctgcaa cacctgttta 2760
tgatcctggc ctacccaagg tctggcttcc ccttgatgca aggtctctgc atcttgagca 2820
gctctgcctc cttgtattcc tctcttgtt ccatgacccc ttaaacccca tccctgcctc 2880
ctggccattg ccatccactg gggatagggg ttctctttgg gacaagaggg ggaggtttca 2940
catatacagg aagaatctgc ttgcttctg agtaggacag gggaactggg agtgggtttt 3000
ccttaaaagg aaagggttta aggatgtgag ggtaaagcggc cagttggggg tttgtttccc 3060
gagcctctca cctccccagc agctgaatgg gaatgctcag gatgcacagc taaccagca 3120
ctcacctgag tgccccgcac aggtatgtgg accgagtgc tgaattcctc cagcaaaagc 3180
tgaagcagtc ccagctgctg gctttgaaga aagagctgat ggtgcagaag cagcaggagg 3240
cacttgagga gcaggcggct ctggagccta agctggacct gctactggag aagaccaagg 3300

```

```

agctgcagaa gctgattgaa gctgacatct ccaagaggta cagcgggagc cctgtgaacc 3360
tgatgggaac ctctctgtga caccctccgt gttcttgccct gcccatcttc tccgcttttg 3420
ggatgaagat gatagccagg gctgttggtt tggggccctt caaggcaaaa gaccaggctg 3480
actggaagat ggaaagccac aggaaggaag cggcacctga tggatgctt ggcactctcc 3540
atgttctcta caagaagctg tggatgattg cctgtgggc taccaggcga aaaccacaga 3600
ttctccttct agttagtata gcggacttaa taaaagagga aaaaactctt gtttcaaaaa 3660
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 3693

```

&lt;210&gt; 40

&lt;211&gt; 230

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 40

```

Met Leu Arg Phe Val Gln Lys Arg Gly Asn Ser Thr Val Tyr Glu Trp
  1              5              10              15

Arg Thr Gly Thr Glu Pro Ser Val Val Glu Arg Pro His Leu Glu Glu
          20              25              30

Leu Pro Glu Gln Val Ala Glu Asp Ala Ile Asp Trp Gly Asp Phe Gly
          35              40              45

Val Glu Ala Val Ser Glu Gly Thr Asp Ser Gly Ile Ser Ala Glu Ala
          50              55              60

Ala Gly Ile Asp Trp Gly Ile Phe Pro Glu Ser Asp Ser Lys Asp Pro
          65              70              75              80

Gly Gly Asp Gly Ile Asp Trp Gly Asp Asp Ala Val Ala Leu Gln Ile
          85              90              95

Thr Val Leu Glu Ala Gly Thr Gln Ala Pro Glu Gly Val Ala Arg Gly
          100             105             110

Pro Asp Ala Leu Thr Leu Leu Glu Tyr Thr Glu Thr Arg Asn Gln Phe
          115             120             125

Leu Asp Glu Leu Met Glu Leu Glu Ile Phe Leu Ala Gln Arg Ala Val
          130             135             140

Glu Leu Ser Glu Glu Ala Asp Val Leu Ser Val Ser Gln Phe Gln Leu
          145             150             155             160

Ala Pro Ala Ile Leu Gln Gly Gln Thr Lys Glu Lys Met Val Thr Met
          165             170             175

Val Ser Val Leu Glu Asp Leu Ile Gly Lys Leu Thr Ser Leu Gln Leu
          180             185             190

Gln His Leu Phe Met Ile Leu Ala Ser Pro Arg Ser Gly Phe Pro Leu
          195             200             205

Met Gln Gly Ser Ala Ile Leu Ser Ser Ser Ala Ser Leu Tyr Ser Ser
          210             215             220

Ser Cys Ser Met Thr Pro
          225             230

```

<210> 41  
 <211> 1701  
 <212> DNA  
 <213> Homo sapiens

<400> 41

```

cccttgagat gattttctct tttcaacttc ttgaacttgg acatgaagga tgtgggcecca 60
gaatcatgtg gccagcccac cccctgttgg ccctcaccag ccttgaggatc tgttctaggg 120
aaggcctccc agcatctggg actcgagagt gggcagcccc tctacctcct ggagctgaac 180
tggggtggaa ctgagtgtgt tcttagctct accgggagga cagctgcctg tttcctcccc 240
accagcctcc tccccacatc cccagctgcc tggctgggtc ctgaagccct ctgtctacct 300
gggagaccag ggaccacagg ccttagggat acaggggggtc cccttctgtt accaccccccc 360
accctcctcc aggacaccac taggtgtgtc tggatgcttg ttctttggcc agccaaggtt 420
cacggcgatt ctccccatgg gatcttgagg gaccaagctg ctgggattgg gaaggagttt 480
caccctgacc gttgccctag ccagggtccc aggaggcctc accatactcc ctttcagggc 540
cagggctcca gcaagcccag ggcaaggatc ctgtgctgct gtctggttga gaggcctgcca 600
ccgtgtgtcg ggagtgtggg ccaggctgag tgcataaggtg acagggccgt gagcatgggc 660
ctgggtgtgt gtgagctcag gcctaggtgc gcagtgtgga gacgggtgtt gtcggggaag 720
aggtgtggct tcaaagtgtg tgtgtgcagg ggggtgggtgt gttagcgtgg gttaggggaa 780
cgtgtgtgcg cgtgctgggt ggcatgtgag atgagtgaact gccggtgaat gtgtccacag 840
ttgagaggtt ggagcaggat gagggaatcc tgtcaccatc aataatcact tgtggagcgc 900
cagctctgcc caagacgcca cctgggcgga cagccaggag ctctccatgg ccaggctgcc 960
tgtgtgcatg ttccctgtct ggtgcccctt tgcccgcctc ctgcaaacct cacagggtcc 1020
ccacacaaca gtgccctcca gaagcagccc ctcgaggcca gaggaaggaa aatggggatg 1080
gctggggctc tctccatect ccttttctcc ttgccttcgc atggctggcc tccccctcca 1140
aaacctccat tcccctgctg ccagcccctt tgccatagcc tgattttggg gaggaggaaag 1200
gggcgatttg agggagaagg ggagaaagct tatggctggg tctggtttct tcccttccca 1260
gaggtcttta ctgttccagg gtggccccag ggcaggcagg ggccacacta tgctgcgcc 1320
ctggtaaagg tgaccctgc catttaccag cagccctggc atgttcctgc cccacaggaa 1380
tagaatggag ggagctccag aaactttcca tcccaaaggc agtctccgtg gttgaagcag 1440
actggatttt tgctctgccc ctgaccctt gtccctcttt gagggagggg agctatgcta 1500
ggactccaac ctcagggact cgggtggcct gcgctagctt cttttgatac tgaaaaactt 1560
taaggtggga ggggtggcaag ggatgtgctt aataaatcaa ttccaagcct caaaaaaaaa 1620
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1680
aaaaaaaaa aaaaaaaaaa a a                                     1701

```

<210> 42  
 <211> 240  
 <212> PRT  
 <213> Homo sapiens

<400> 42

```

Met Lys Asp Val Gly Pro Glu Ser Cys Gly Gln Pro Thr Pro Cys Trp
  1             5             10             15

Pro Ser Pro Ala Leu Glu Ser Val Leu Gly Lys Ala Ser Gln His Leu
          20             25             30

Gly Leu Glu Ser Gly Gln Pro Leu Tyr Leu Leu Glu Leu Asn Trp Gly
          35             40             45

Gly Thr Glu Cys Val Leu Ser Ser Thr Gly Arg Thr Ala Ala Cys Phe
          50             55             60

Leu Pro Thr Ser Leu Leu Pro Thr Ser Pro Ala Ala Trp Leu Gly Pro
          65             70             75             80

Glu Ala Leu Cys Leu Pro Gly Arg Pro Gly Thr Thr Gly Leu Arg Asp
          85             90             95

```

Thr Gly Gly Pro Leu Leu Leu Pro Pro Pro Thr Leu Leu Gln Asp Thr  
 100 105 110

Thr Arg Trp Cys Trp Met Leu Val Leu Trp Pro Ala Lys Val His Gly  
 115 120 125

Asp Ser Pro His Gly Ile Leu Arg Asp Gln Ala Ala Gly Ile Gly Lys  
 130 135 140

Glu Phe His Pro Asp Arg Cys Pro Ser Gln Val Pro Arg Arg Pro His  
 145 150 155 160

His Thr Pro Phe Gln Gly Gln Gly Ser Ser Lys Pro Arg Ala Arg Ile  
 165 170 175

Leu Cys Cys Cys Leu Val Glu Ser Leu Pro Pro Cys Val Gly Ser Val  
 180 185 190

Gly Gln Ala Glu Cys Ile Gly Asp Arg Ala Val Ser Met Gly Leu Gly  
 195 200 205

Val Cys Glu Leu Arg Pro Arg Cys Ala Val Trp Arg Arg Val Leu Ser  
 210 215 220

Gly Lys Arg Cys Gly Phe Lys Val Cys Val Cys Arg Gly Trp Val Cys  
 225 230 235 240

&lt;210&gt; 43

&lt;211&gt; 1784

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 43

aggctctagaa ttcaatcggg aatatctttt aagtttttaa aaaactggaa taatttatatc 60  
 tatctttttt gccgtttata tttaggggtt ttgttgata aaatcaagtc ttggttgttg 120  
 ctgtctgaat taaatattta tgagtgggtc atttttaagt atagtgaaca agacaccata 180  
 ttaagtacag tgataaaagca tctatattct gtaaaaaaaaa aaaaaatctg cctatgcatg 240  
 ttttttaaga aaaaaaaaaat ggctgtatcg gcctgtatgg gactgtaatg cgcttagtgg 300  
 tctgacatat actggaaatg tatgtatact ggcgtacttt atattctcta aaatgcttaa 360  
 tgcctttgaa attttgtaat caaaaaaaag ctttgaaaaa tctaaagggg agagtattct 420  
 ttaaagtttt taacataagc ttgtcaatgc acatgtagat ggtagcatg tttagcaaac 480  
 ctgtgaaat tataataagt ttgtagttac atgtgaaact ctaaatgcat ggcaactgtt 540  
 aatgtcataa cagtttagtt attttgttct gttctgtcat gtgccacaaa atatgtactt 600  
 ttttcacttt tttccctttg tatatcagtt acgggttaca actggttcat tctgaaaaca 660  
 acaacaacaa aagtccattc atatttttta acaattgtat aagtgcccaa gtaattcact 720  
 acagcctaaa gccttgccct tgaatttga cttctgacat gttggcaatc aaagcatgca 780  
 ctgttaacaa tgaaaaagaa aaagcatttt atattactac tcaataaaat gtgcatgaac 840  
 ttacagaatt ctcaccttc cactgagtc gctgaaggga tttatgtgca caaccaccat 900  
 gtgtcttcta ggtgctggcc caccaccaca catcacaggc tgatttccac aggtcttctc 960  
 ctaggggcct cgtgatctga ggggtggtgc ctacttccac tgtaagaaag aatcttggtg 1020  
 gatttgtgtc tcaaatcaga taagagaagc ctgtttaaag agcagatgcc atcttctggc 1080  
 ttcctcaagg agccagttaa aaaccagag cattcctttt tattgaaaaa taaaattaat 1140  
 ttgttatcag gttgtttcag ttgtattgga tgccctatct atctgctaaa gcaaaaagta 1200  
 ctaggctact aagtgcattt tcatcacaga aaagagttgc atttgtatta acaagaaatt 1260  
 tgtataccca cgcttcagct actatctaact catcacccga agatttaaga tacaccaa 1320  
 ttcagtttgt ttgtaacatt gttcatcttt agtgcacttt gttttatata ataaagtatg 1380  
 cctgttatat taaataataa gaatatggca attagcgata tagcatatcc aaacaaagat 1440  
 gttctcgata cagtctggca aagactatcc caagggtatt ttaatgaatt cagacatttt 1500  
 ttctctgtgga tattttctca tctaaaaaaa agtggaacc aaggaaaata ttagatgca 1560

acttactaga gtgatgatgt gaaagaaatg gtgattctgg tatcatgggtg tttattttct 1620  
 ttcttataac tgcagagaaa atatcctgac taaaaaaaaat tcattttttt ggattccttt 1680  
 cttttacaaa ttgtgctgag gcaactatgg catagaaata aacatttgac attaaaaataa 1740  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1784

<210> 44  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens

<400> 44  
 Met Cys His Lys Ile Cys Thr Phe Phe Thr Phe Phe Pro Leu Tyr Ile  
 1 5 10 15  
 Ser Tyr Gly Leu Gln Leu Val His Ser Glu Asn Asn Asn Asn Lys Ser  
 20 25 30  
 Pro Phe Ile Phe Phe Asn Asn Cys Ile Ser Ala Gln Val Ile His Tyr  
 35 40 45  
 Ser Leu Lys Pro Cys Leu Cys Asn Leu Thr Ser Asp Met Leu Ala Ile  
 50 55 60  
 Lys Ala Cys Thr Cys Asn Asn Glu Lys Glu Lys Ala Phe Tyr Ile Thr  
 65 70 75 80  
 Thr Gln

<210> 45  
 <211> 1034  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (598)

<400> 45  
 ggaagatggc ggcctctggg gcggagccgc aggtcctggt acaatacttg gtgttacgaa 60  
 aggatctatc acaagctccg ttctcctggc cggcgggccc actggttagcg caggcttgtc 120  
 acgcgccac cgcgcccttg cacactcacc gcgaccaccc gcacacagcc gcttacctcc 180  
 aagagctggg gcgcatgccc aaagtgggtc tcgaggcccc agatgagacc accctaaagg 240  
 agctggccga gacctgcaa cagaagaaca ttgaccacat gctgtggctt gagcaaccag 300  
 agaatatcgc cacttgattt gctctccggc cctaccccaa ggaagaagtg ggccagtatt 360  
 tgaagaagtt cggattgttc aagtaactgc tgctttgatg tgtttgaata cgcaggccac 420  
 ccattccaaa gcatcatgtg ttctctgcag tgtcagcttg ctcccgctctt tcagttgtga 480  
 caatttcttg aggtttaagc acatgttcat attaaagttg tcattaataa ctacttcctc 540  
 ttattaataa gttcaagtgg ggaagggtgg agagcagtat tgtctgggga tcattgcnc 600  
 aatagaagat ttggttagac tctcctgttg ggctcaagga aactcccttc cagtcactcg 660  
 gggttgaaac tttgcttttg aattccttct tattcacatc cagttatcat atttcattga 720  
 atccaagata acctcaactt caagatgcgg tagtatttta tgtattgtta aaaaatatgc 780  
 cggcaaatta aacatttgta tttcaataac aaagatgtta aaatttggcc agtgtggtgg 840  
 ctacacatcg ttaattccag gggtttggga agccaaggca ggaggatcgc ttgagcccat 900  
 gagttcaagg ttacagtcag ttctaatacag gccacgcgac tccagcgtgg gcaacagagt 960  
 gagacacggg ttctataaag attaataaca agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1020  
 aaaaaaaaaa aaaa 1034

<210> 46



<211> 126  
 <212> PRT  
 <213> Homo sapiens

<400> 46

```

Met Ala Ala Ser Gly Ala Glu Pro Gln Val Leu Val Gln Tyr Leu Val
  1             5             10             15

Leu Arg Lys Asp Leu Ser Gln Ala Pro Phe Ser Trp Pro Ala Gly Ala
      20             25             30

Leu Val Ala Gln Ala Cys His Ala Ala Thr Ala Ala Leu His Thr His
      35             40             45

Arg Asp His Pro His Thr Ala Ala Tyr Leu Gln Glu Leu Gly Arg Met
      50             55             60

Arg Lys Val Val Leu Glu Ala Pro Asp Glu Thr Thr Leu Lys Glu Leu
      65             70             75             80

Ala Glu Thr Leu Gln Gln Lys Asn Ile Asp His Met Leu Trp Leu Glu
      85             90             95

Gln Pro Glu Asn Ile Ala Thr Cys Ile Ala Leu Arg Pro Tyr Pro Lys
      100            105            110

Glu Glu Val Gly Gln Tyr Leu Lys Lys Phe Arg Leu Phe Lys
      115            120            125

```

<210> 47  
 <211> 1626  
 <212> DNA  
 <213> Homo sapiens

<400> 47

```

caacttgtgt agctgaaggt ttgtttgtga cttattacag agcctgtgac ttaaaaatcc 60
ttcccacaac cacaagctaa agtgggagaa gacaaactac ctcacctttt caaccaagag 120
ggaggagcaa aatcagtgta acttttacag aagaacctgc cagcctgtga tgatcctacc 180
aaagagaaaac ctcaatgagt tatggaattt ccttttttgt gaattgagtg ctgtttttgc 240
ttttctcaga ttccaaatga gagtatacat tttcttttgt ttgatgtgct gggtgagatc 300
tgataataaa agaccatgcc ttgaattctc tcagctaagt gtaaaggatt ccttcagaga 360
tttatttatt ccgagaatag agaccattct gatgatgtat acaaggaaca acctaaactg 420
tgctgagcca ctgtttgaac aaaataactc acttaatgtt aatttcaaca cacaaaagaa 480
aacagtcctgg cttattcacg gatacagacc agtaggctcc atcccattat ggcttcagaa 540
cttcgtaagg attttgctga atgaagaaga tatgaatgta attgtagtag actggagccg 600
gggtgctaca acttttattt ataatagagc agttaaaaac accagaaaag ttgctgtgag 660
tttgagtgtg cacattaata atcttttgaa gcatggtgca tctcttgaca attttcattt 720
catagggtgtg agtttagggg ctcatatcag tggatttgtt ggaaagatat ttcattggtca 780
acttggaaga ataacaggtc ttgacctgc tgggccaagg ttctccagaa aaccaccata 840
tagcagatta gattacacgg atgcaaagtt tgtggatgtc atccattctg actccaatgg 900
aattcaattc attaaatgca accaccagag agcagttcac ttgttcatgg catctttaga 960
aacaactgc aattttattt catttcttg tcgttcatac aaagattaca agactagctt 1020
atgtgtggac tgtgactgtt ttaaggaaaa atcatgtcct cggctgggtt atcaagccaa 1080
gctattttaa ggtgttttaa aagaaaggat ggaaggaaaga cctcttagga cactgtgtt 1140
tttgataaca agtgcctatt attttgttct cagtataatt gttccagata aaactatgat 1200
ggatggctcg ttttcattta aattattaaa tcagcttggga atgattgaag agccaaggct 1260
ttatgaagaa agataacata tgtaaagag gcacccttac tctaaacaac tagtgacttt 1320
aaaagtctta agcgtatcag gagatggaga ccatcctggc taacatggtg aaacctgtc 1380
tctactaaaa attcagaaaa ttgactgggc atgggtggcac gtgcctgtag tcccagctac 1440

```

tcaggaggct gaggcaagag aattgcttga acccaggagg tggaggttgc agtgagctga 1500  
 gattgcaccg ctgccctcca gcctgggtga cagagcaaga ctccatttca aataaataaa 1560  
 taaataaata aataaataaa taaataaata aataaataaa gttaaagagt aaaaaaaaaa 1620  
 aaaaaa 1626

<210> 48

<211> 368

<212> PRT

<213> Homo sapiens

<400> 48

Met Ile Leu Pro Lys Arg Asn Leu Asn Glu Leu Trp Asn Phe Leu Phe  
 1 5 10 15  
 Gly Glu Leu Ser Ala Val Phe Ala Phe Leu Arg Phe Gln Met Arg Val  
 20 25 30  
 Tyr Ile Phe Leu Cys Leu Met Cys Trp Val Arg Ser Asp Asn Lys Arg  
 35 40 45  
 Pro Cys Leu Glu Phe Ser Gln Leu Ser Val Lys Asp Ser Phe Arg Asp  
 50 55 60  
 Leu Phe Ile Pro Arg Ile Glu Thr Ile Leu Met Met Tyr Thr Arg Asn  
 65 70 75 80  
 Asn Leu Asn Cys Ala Glu Pro Leu Phe Glu Gln Asn Asn Ser Leu Asn  
 85 90 95  
 Val Asn Phe Asn Thr Gln Lys Lys Thr Val Trp Leu Ile His Gly Tyr  
 100 105 110  
 Arg Pro Val Gly Ser Ile Pro Leu Trp Leu Gln Asn Phe Val Arg Ile  
 115 120 125  
 Leu Leu Asn Glu Glu Asp Met Asn Val Ile Val Val Asp Trp Ser Arg  
 130 135 140  
 Gly Ala Thr Thr Phe Ile Tyr Asn Arg Ala Val Lys Asn Thr Arg Lys  
 145 150 155 160  
 Val Ala Val Ser Leu Ser Val His Ile Lys Asn Leu Leu Lys His Gly  
 165 170 175  
 Ala Ser Leu Asp Asn Phe His Phe Ile Gly Val Ser Leu Gly Ala His  
 180 185 190  
 Ile Ser Gly Phe Val Gly Lys Ile Phe His Gly Gln Leu Gly Arg Ile  
 195 200 205  
 Thr Gly Leu Asp Pro Ala Gly Pro Arg Phe Ser Arg Lys Pro Pro Tyr  
 210 215 220  
 Ser Arg Leu Asp Tyr Thr Asp Ala Lys Phe Val Asp Val Ile His Ser  
 225 230 235 240  
 Asp Ser Asn Gly Ile Gln Phe Ile Lys Cys Asn His Gln Arg Ala Val  
 245 250 255  
 His Leu Phe Met Ala Ser Leu Glu Thr Asn Cys Asn Phe Ile Ser Phe

260                      265                      270  
 Pro Cys Arg Ser Tyr Lys Asp Tyr Lys Thr Ser Leu Cys Val Asp Cys  
       275                      280                      285  
 Asp Cys Phe Lys Glu Lys Ser Cys Pro Arg Leu Gly Tyr Gln Ala Lys  
       290                      295                      300  
 Leu Phe Lys Gly Val Leu Lys Glu Arg Met Glu Gly Arg Pro Leu Arg  
       305                      310                      315                      320  
 Thr Thr Val Phe Leu Asp Thr Ser Ala Tyr Tyr Phe Val Leu Ser Ile  
                               325                      330                      335  
 Ile Val Pro Asp Lys Thr Met Met Asp Gly Ser Phe Ser Phe Lys Leu  
                               340                      345                      350  
 Leu Asn Gln Leu Gly Met Ile Glu Glu Pro Arg Leu Tyr Glu Glu Arg  
                               355                      360                      365

<210> 49  
 <211> 1221  
 <212> DNA  
 <213> Homo sapiens

<400> 49  
 ggaaaagctg agaataatca cctctgataa agatcacaga agctgcccgg gaggtgtttg 60  
 attaaattca tgtattgaaa atattgttca gaccccatgt gacataactg gagccagtgc 120  
 agtgccatga agaactacga gattagcctg gatattaact tgtcttctag agaatagatt 180  
 tcatgttcca ttcttctgca atggttaatt cacacagaaa accaatgttt aacattcaca 240  
 gaggatttta ctgcttaaca gccatcttgc ccaaatatg catttgttct cagttctcag 300  
 tgccatctag ttatcacttc actgaggatc ctggggcctt cccagtagcc actaatgggg 360  
 aacgatttcc ttggcaggag ctaaggctcc ccagtgtggt cattectctc cattatgacc 420  
 tctttgtcca cccaatctc acctctctgg actttgttgc atctgagaag atcgaagtct 480  
 tggtcagcaa tgctacccag tttatcatct tgcacagcaa agatcttgaa atcacgaatg 540  
 ccacccttca gttagaggaa gattcaagat acatgaaacc aggaaaagaa ctgaaagtgt 600  
 tgagttaccc tgctcatgaa caaattgcac tgctgggtcc agagaaactt acgcctcacc 660  
 tgaataacta tgtggctatg gacttccaag ccaagttagg tgatggcttt gaagggtttt 720  
 ataaaagcac atacagaact cttggtggtg aaacaagaat tcttgcagta acagattttg 780  
 agccaaccca ggcacgcatg gctttccctt gctttgatga accgttgctc aaagccaact 840  
 tttcaatcaa gatacgaaga gagagcaggc atattgcact atccaacatg ccaaggtgt 900  
 ccatctatgc atccccagac aaacggaatc aaacacatta tgctttgcag gcatcactga 960  
 agctacttga tttttatgaa aagtactttg atatctacta tccactctcc aaactgggta 1020  
 tgttcaaatt ccacattatt gtcttcattt ttgctcataa aacttgctta gatctcttcc 1080  
 ctctttctct ttgtatgtga tttaaatgag cactgaggaa ttcagttagc tcaggaaaaa 1140  
 ataatttggt cctcagagat gattcttgag tgtagaaaat aaaatattta tgacatgccc 1200  
 caaaaaaaaa aaaaaaaaaa a 1221

<210> 50  
 <211> 305  
 <212> PRT  
 <213> Homo sapiens

<400> 50  
 Met Phe His Ser Ser Ala Met Val Asn Ser His Arg Lys Pro Met Phe  
       1                      5                      10                      15  
 Asn Ile His Arg Gly Phe Tyr Cys Leu Thr Ala Ile Leu Pro Gln Ile  
                               20                      25                      30

Cys Ile Cys Ser Gln Phe Ser Val Pro Ser Ser Tyr His Phe Thr Glu  
           35                          40                          45  
 Asp Pro Gly Ala Phe Pro Val Ala Thr Asn Gly Glu Arg Phe Pro Trp  
           50                          55                          60  
 Gln Glu Leu Arg Leu Pro Ser Val Val Ile Pro Leu His Tyr Asp Leu  
           65                          70                          75                          80  
 Phe Val His Pro Asn Leu Thr Ser Leu Asp Phe Val Ala Ser Glu Lys  
                           85                          90                          95  
 Ile Glu Val Leu Val Ser Asn Ala Thr Gln Phe Ile Ile Leu His Ser  
                           100                          105                          110  
 Lys Asp Leu Glu Ile Thr Asn Ala Thr Leu Gln Ser Glu Glu Asp Ser  
           115                          120                          125  
 Arg Tyr Met Lys Pro Gly Lys Glu Leu Lys Val Leu Ser Tyr Pro Ala  
           130                          135                          140  
 His Glu Gln Ile Ala Leu Leu Val Pro Glu Lys Leu Thr Pro His Leu  
           145                          150                          155                          160  
 Lys Tyr Tyr Val Ala Met Asp Phe Gln Ala Lys Leu Gly Asp Gly Phe  
                           165                          170                          175  
 Glu Gly Phe Tyr Lys Ser Thr Tyr Arg Thr Leu Gly Gly Glu Thr Arg  
                           180                          185                          190  
 Ile Leu Ala Val Thr Asp Phe Glu Pro Thr Gln Ala Arg Met Ala Phe  
           195                          200                          205  
 Pro Cys Phe Asp Glu Pro Leu Phe Lys Ala Asn Phe Ser Ile Lys Ile  
           210                          215                          220  
 Arg Arg Glu Ser Arg His Ile Ala Leu Ser Asn Met Pro Lys Val Ser  
           225                          230                          235                          240  
 Ile Tyr Ala Ser Pro Asp Lys Arg Asn Gln Thr His Tyr Ala Leu Gln  
                           245                          250                          255  
 Ala Ser Leu Lys Leu Leu Asp Phe Tyr Glu Lys Tyr Phe Asp Ile Tyr  
           260                          265                          270  
 Tyr Pro Leu Ser Lys Leu Gly Met Phe Lys Phe His Ile Ile Val Phe  
           275                          280                          285  
 Ile Phe Ala His Lys Thr Cys Leu Asp Leu Phe Pro Leu Ser Leu Cys  
           290                          295                          300  
 Met  
 305

&lt;210&gt; 51

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 51

```

ggtagggtagc gagtctgagg ccgttccgc ggcctcctcc tcctcccgt tcccttcacc 60
ccccccgc acccctttcc ccatcccgcc tccgtcacc tcccgcccc cacactcagg 120
acaagaatgc cctgcccga acaaccagc agcgctaga tggctttggt cacgggtccag 180
cggtcaccta cccccagcac cacctccagc cctgcgcc cggaggcaga cagtggggag 240
gaagaatgcc ggtcacagcc caggagcatc agcgagagct ttctaactgt caaagggtgt 300
gccctttttc taccacgggg aaatgggtca tccacaccaa gaatcagcca cagacggaac 360
aagcatgcag gcgatctcca acagcatctc caagcaatgt tcattttact ccgccagaa 420
gacaacatca ggctgggtgt aagactggaa agtacttacc agaatcgaac acgctatatg 480
gtagtgggtt caactaatgg tagacaagac actgaagaaa gcacgtcctt aggaatggat 540
ttctcctcta atgacagcac ttgtaccatg ggcttagttt tgctctctg gagcgacacg 600
ctaattcatt tggatgggtga tggtaggttc agtgatcga cggataacag agttcacata 660
ttcaaacctg tatctgtgca ggcaatgtgg gttgacaggg attcaaggaa caaacactgt 720
gatgtactat tggtaggaaga atgaactgga gcagcctttc tggagagtga tttgccaata 780
tgcttatca ttttgcata tctttgtcct agtaactcta tttctatgga tttactctaa 840
gtttgtaaac atggatgtgt gcaaagattt tagctctaag aatgtttgtc agtgttctaa 900
taatatgaaa aaataaaaaa caaatgattg aaaaataaaa aaaaaaaaaa a 951

```

&lt;210&gt; 52

&lt;211&gt; 194

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 52

```

Met Ala Leu Val Thr Val Gln Arg Ser Pro Thr Pro Ser Thr Thr Ser
  1                      5                      10                      15

Ser Pro Cys Ala Ser Glu Ala Asp Ser Gly Glu Glu Glu Cys Arg Ser
          20                      25                      30

Gln Pro Arg Ser Ile Ser Glu Ser Phe Leu Thr Val Lys Gly Ala Ala
      35                      40                      45

Leu Phe Leu Pro Arg Gly Asn Gly Ser Ser Thr Pro Arg Ile Ser His
  50                      55                      60

Arg Arg Asn Lys His Ala Gly Asp Leu Gln Gln His Leu Gln Ala Met
  65                      70                      75                      80

Phe Ile Leu Leu Arg Pro Glu Asp Asn Ile Arg Leu Ala Val Arg Leu
          85                      90                      95

Glu Ser Thr Tyr Gln Asn Arg Thr Arg Tyr Met Val Val Val Ser Thr
      100                      105                      110

Asn Gly Arg Gln Asp Thr Glu Glu Ser Ile Val Leu Gly Met Asp Phe
      115                      120                      125

Ser Ser Asn Asp Ser Thr Cys Thr Met Gly Leu Val Leu Pro Leu Trp
      130                      135                      140

Ser Asp Thr Leu Ile His Leu Asp Gly Asp Gly Gly Phe Ser Val Ser
      145                      150                      155                      160

Thr Asp Asn Arg Val His Ile Phe Lys Pro Val Ser Val Gln Ala Met
          165                      170                      175

Trp Val Asp Arg Asp Ser Arg Asn Lys His Cys Asp Val Leu Leu Val
          180                      185                      190

```

Glu Glu

<210> 53  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 53  
 gcatgatatt ttacggttc acccatattg catgtatcag gaatataatc ctttttatta 60  
 ttgagtagtg ttctattgta tgtatatacc acagtttatt tctcccttca tcctttgcta 120  
 gattttgggg ttttttcaca ttgcgtatt cagtataaac ctgctctcaa cattcatgtg 180  
 caagtctttg agtggacata tatttgctt tctcttgagt gaatgcacct tgttgggtca 240  
 cgtggcttaa cttaaaaaaa ttttaatac tgtggtgcat atgtagtgat tattagtgat 300  
 tatctcataa ttttattttc ttgtttaatg atgttgagtg tatttcattt gtatttttagt 360  
 ttgcaaagt ttgttcaa tcttcacctg tttttaatga agacgtacga cttatttttg 420  
 tgttctgaac ataagttctt tgtcacataa aatgtgctat gaatgttgag ttttaaatac 480  
 tccaaatgaa tggctagaga attactattt gtagaaatat ttatatgtca aagggatgct 540  
 aacaatttac tttattgctc taaaatagaa aagttgccag aatgctgtgg agtttttagt 600  
 gaaaacatga tagctggtgt tactgagtaa atttgagtgt taaatgtcaa tgtaagctaa 660  
 cggccaagat agggaccact gcagggtggt tacttgacgc tgtgactcaa ctggctcttc 720  
 actgccaaac atacctgggg ttggatcatt ggcctgacgt ttgcaaattg aggaacctta 780  
 gggcaaatca gtgaacttct gaactgcctt cgtcttcagt tatatgggga tttccctact 840  
 tttgagatcc ttgtaaggat tatatgagat gaagagatga gacaaggat ataaaagtcc 900  
 tagcacagag cgtgtcatat aatatggctt cacaagtacc ctcatctctt ttcagtcgt 960  
 tttttgtttt tgtttttggt tttttgagac catctcactc tgttgcccag gctggagtgc 1020  
 ctcttcattt ttatttcttt attcagcaag tattgatcaa atgtgctttg taccaggtag 1080  
 tgagctcttc gttgggat atgtgtgac aaggagattg tagattctgg cagggaaaac 1140  
 tgacatcaaa cacggcgacc cgacatagtg agacctgtc tctactagaa gaactttaaa 1200  
 aatcacctag gtgtgggccc ggcacggtg ctaacgcctg tgggtcccag actttgggat 1260  
 gctgaggcgg gtggatcacg gggtcaggag atcgagacca tcctggataa cagggagaaa 1320  
 ccccgctctt actggaaata caaggaaatt ggccgggctg gggggcgggc atctgtggtc 1380  
 ccaattactc gggaggctgc agcaggagag tggcatgaac cggggaggcg gatcttgcac 1440  
 tgagccgaga tcacgccact gcactccagc ctgggcgaca gaatgagact ccatctcaaa 1500  
 aaaaaaaaaa aaaa 1514

<210> 54  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

<400> 54  
 Met Ala Ser Gln Val Pro Ser Ser Pro Phe Gln Ser Phe Phe Val Phe  
 1 5 10 15  
 Val Phe Val Phe Leu Arg Pro Ser His Ser Val Ala Gln Ala Gly Val  
 20 25 30  
 Pro Leu His Phe Tyr Phe Phe Ile Gln Gln Val Leu Ile Lys Cys Ala  
 35 40 45  
 Leu Tyr Gln Val Leu Ser Ser Ser Leu Gly Tyr Asn Gly Asp Gln Gly  
 50 55 60  
 Asp Cys Arg Phe Trp Gln Gly Lys Leu Thr Ser Asn Thr Ala Thr Arg  
 65 70 75 80  
 His Ser Glu Thr Leu Ser Leu Leu Glu Glu Leu

85

90

<210> 55  
 <211> 1417  
 <212> DNA  
 <213> Homo sapiens

<400> 55  
 gtccaaatcc tattgtccac agtcagactt ctacaacctc ctctgaacaa atgcagcctc 60  
 caatgtttca ctctcaaagt accattgctg tgttacaggg ctcttcagtt cctcaagacc 120  
 agcagtcaac caacatattt ctttcccaga gtcccatgaa taatcttcag actaacacag 180  
 tagcccaaga agcatttttt gcagcaccga actcaatttc tccacttcag tcaacatcaa 240  
 acagtgaaca acaagctgct ttccaacagc aagctccaat atcacacatc cagactccta 300  
 tgctttccca agaacaggca caaccccgc agcaggggtt atttcagcct caggtggccc 360  
 tgggctccct tccaccta atcgaatgcctc aaagccaaca aggaaccatg ttccagtcac 420  
 agcactcaat agttgccatg cagagtaact ctccatccca ggaacagcag cagcagcagc 480  
 aacagcagca gcaacagcag cagcaacaac aacagagcat tttattcagt aatcagaata 540  
 ccatggctac aatggcgtct ccaagcaac caccaccaa catgatattc aacccaaatc 600  
 aaaatccaat ggctaatacag gagcaacaga accagtcaat ttttcacaa caaagtaaca 660  
 tggccccaat gaatcaagag caacagccca tgcaatttca gagtcatgcc acagtttcct 720  
 cacttcagaa cccaggtcct acccagtcgg aatcatcaca gaccccttg ttccatagct 780  
 ctccctcagat tcagttggta caagggtcac ctagtcttca agagcagcaa gtaactctct 840  
 tcttatctcc agcatccatg tctgccttgc agaccagtat aaatcaacaa gatatgcaac 900  
 agtctcctct ttattcccct cagaacaaca tgcctggaat tcaaggagcc acattttcgc 960  
 ctcaaccaca ggctacttta tttcacaaca cagcaggagg cacaatgaac caactgcaga 1020  
 attctcctgg ctcatctcag cagacatcag gaatgttctt atttggcatt caaaataact 1080  
 gtagtcagct ttttaacctct ggaccagcta cattgcctga tcagttagtg gccataagtc 1140  
 agccaggcca accacaaaac gagggccagc cacctgtgac aacacttctt tctcagcaaa 1200  
 tgccagagaa ttctccactg gcatcctcta taaacaccaa ccagaacatc gaaaagattg 1260  
 atttgcttgt ttcatgcaa aaccaaggga acaacttgac tggctccttt taactggata 1320  
 taaattccac gaagaaaatc ctgattccaa gatgtcctga gatcttgggg ttccatgaga 1380  
 attattactt taaaaacaaa acaaaaaaaaa aaaaaaa 1417

<210> 56  
 <211> 420  
 <212> PRT  
 <213> Homo sapiens

<400> 56  
 Met Gln Pro Pro Met Phe His Ser Gln Ser Thr Ile Ala Val Leu Gln  
 1 5 10 15  
 Gly Ser Ser Val Pro Gln Asp Gln Gln Ser Thr Asn Ile Phe Leu Ser  
 20 25 30  
 Gln Ser Pro Met Asn Asn Leu Gln Thr Asn Thr Val Ala Gln Glu Ala  
 35 40 45  
 Phe Phe Ala Ala Pro Asn Ser Ile Ser Pro Leu Gln Ser Thr Ser Asn  
 50 55 60  
 Ser Glu Gln Gln Ala Ala Phe Gln Gln Gln Ala Pro Ile Ser His Ile  
 65 70 75 80  
 Gln Thr Pro Met Leu Ser Gln Glu Gln Ala Gln Pro Pro Gln Gln Gly  
 85 90 95  
 Leu Phe Gln Pro Gln Val Ala Leu Gly Ser Leu Pro Pro Asn Pro Met  
 100 105 110

Pro Gln Ser Gln Gln Gly Thr Met Phe Gln Ser Gln His Ser Ile Val  
 115 120 125  
 Ala Met Gln Ser Asn Ser Pro Ser Gln Glu Gln Gln Gln Gln Gln  
 130 135 140  
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ser Ile Leu Phe Ser  
 145 150 155 160  
 Asn Gln Asn Thr Met Ala Thr Met Ala Ser Pro Lys Gln Pro Pro Pro  
 165 170 175  
 Asn Met Ile Phe Asn Pro Asn Gln Asn Pro Met Ala Asn Gln Glu Gln  
 180 185 190  
 Gln Asn Gln Ser Ile Phe His Gln Gln Ser Asn Met Ala Pro Met Asn  
 195 200 205  
 Gln Glu Gln Gln Pro Met Gln Phe Gln Ser Gln Ser Thr Val Ser Ser  
 210 215 220  
 Leu Gln Asn Pro Gly Pro Thr Gln Ser Glu Ser Ser Gln Thr Pro Leu  
 225 230 235 240  
 Phe His Ser Ser Pro Gln Ile Gln Leu Val Gln Gly Ser Pro Ser Ser  
 245 250 255  
 Gln Glu Gln Gln Val Thr Leu Phe Leu Ser Pro Ala Ser Met Ser Ala  
 260 265 270  
 Leu Gln Thr Ser Ile Asn Gln Gln Asp Met Gln Gln Ser Pro Leu Tyr  
 275 280 285  
 Ser Pro Gln Asn Asn Met Pro Gly Ile Gln Gly Ala Thr Phe Ser Pro  
 290 295 300  
 Gln Pro Gln Ala Thr Leu Phe His Asn Thr Ala Gly Gly Thr Met Asn  
 305 310 315 320  
 Gln Leu Gln Asn Ser Pro Gly Ser Ser Gln Gln Thr Ser Gly Met Phe  
 325 330 335  
 Leu Phe Gly Ile Gln Asn Asn Cys Ser Gln Leu Leu Thr Ser Gly Pro  
 340 345 350  
 Ala Thr Leu Pro Asp Gln Leu Met Ala Ile Ser Gln Pro Gly Gln Pro  
 355 360 365  
 Gln Asn Glu Gly Gln Pro Pro Val Thr Thr Leu Leu Ser Gln Gln Met  
 370 375 380  
 Pro Glu Asn Ser Pro Leu Ala Ser Ser Ile Asn Thr Asn Gln Asn Ile  
 385 390 395 400  
 Glu Lys Ile Asp Leu Leu Val Ser Leu Gln Asn Gln Gly Asn Asn Leu  
 405 410 415  
 Thr Gly Ser Phe  
 420



<210> 57  
 <211> 2297  
 <212> DNA  
 <213> Homo sapiens

<400> 57  
 gaagtgaggg ttgaatgatc cccacttaac taaaaaatga ataagcgtag ttgaaatgat 60  
 ttttttaaagt gtttggtagt ctatacttat gttctttctt tgtttccact atagacagta 120  
 ttcgtgggcta ctttggggaa acaattgtct tgtaactttg atttttggag tatttcactt 180  
 ttgcattaat ccccatggct gtcattgggt taccttacta cttgtttgtg tgggaagact 240  
 atgacaagta cgtgatcttt gcctcgttca acctcatctg gtccacgggtg attctggaac 300  
 tgtggaagcg tggctgtgcc aacatgacct acaggtgggg gacactgctc atgaagagaa 360  
 agtttgagga gccccggcca ggatttcatg gtgtcttggg tatcaattcc atcactggga 420  
 aggaggagcc tctgtacccc agctacaaga gacagttgcg catttacctg gtctccctgc 480  
 cattcgtgtg cctctgcctc tatttctcac tgtatgtcat gatgatttac ttcgacatgg 540  
 aggtttgggc cttgggtcta catgagaaca gcggtctga gtggaccagt gtctgttgtt 600  
 atgtgcccg catcatctat gccattgtga ttgagatcat gaatcgtctc tatcgatatg 660  
 ctgccgagtt tttaacttca tgggagaatc acagattgga atctgcctat cagaaccatc 720  
 taattctgaa agtttttagtg ttcaacttcc tcaattgctt tgcctcactc ttctatatg 780  
 cctttgtctt gaaagatatg aagcttttgc gccagagctt ggccactctc ctaattacct 840  
 ccagatcct caaccaaatt atggaatctt ttcttctta ttggctccaa aggaagcatg 900  
 gtgtgcaggt gaagaggaag gtgcaggctt taaaggcaga cattgatgct acattatatg 960  
 aacaagtcac cctggaaaaa gaaatgggaa cttatttggg cacctttgat gattacttgg 1020  
 agttattcct gcagtttggg tatgtgagcc ttttctcctg tgtttaccca ttagcagctg 1080  
 cctttgctgt gttaataaac ttcactgaag taaattcaga tgccttaaaa atgtgcaggg 1140  
 tcttcaaacg tccattctca gaaccttcag ccaatattgg tgtgtggcag atgatatttt 1200  
 gtttgacac aggtgtaaag agagggctga attgcaagg catgaggaat cttttggggg 1260  
 aaatggaaat gtctgtgtc ttgtttgtgg tgggtgtggg ttcacaggta aatacaccta 1320  
 tcaaaaggta atgaagtata taccttaaat gcatgcagtt tattgtatgt aaattataac 1380  
 tcaatatagg tgatttttaa aaaaacctga aagtttagtt acaaacatat tgcaagttca 1440  
 ggaagccagg cactgtcata tgctgtgtg ggaagcatga gctggtcaac ccatggagtg 1500  
 cagcttcgta tttatctatc aaaattacaa atgcatgtcc cctttgactc agccatttca 1560  
 ctttccagaa tttagcctaa ttccacattt gttaaatgat gtacttataa gatcaccaat 1620  
 tgtagcactg tttgtaatag caactaaatg cccaccaata agaaaatggg tacataaatt 1680  
 ctgatacgtc catgtaataa aatgcagaag cagtgtggca aagaatgagg gagctctttt 1740  
 agtattgaca cagaaagtcc ctcaagacac tttaaatgac taaagcaagg ggcctgacag 1800  
 tatgtagtat gctgaaaagg gagtaggaaa gagtgtatat attcaatatg cttattttgc 1860  
 atacaaactg tctggaagaa tacataagaa attgcaaata gtgggtgtct tctagggaga 1920  
 atgggagctg cgaagtggaa gaaaagggga caagggaaaa agacactctt cactatgtac 1980  
 ttagaatttt ttatttttaa gccatgagaa tataatcaaa agtaaataaa tagaaatttt 2040  
 aaactaaagt aaagacagtc ttagatttct tatgaagaaa actgtggaaa aataatcaga 2100  
 ctacacaaag atttctaaat tgtaagatgg cagaagttct ccatgggaca aaatgtattc 2160  
 atattaagtt tggattcagt catcttttgt tttgcttctt ttaaaattaa tgtttctaat 2220  
 agtacttggt tttcttggaa ttaatgggta aattattaag tggtagtcac catatacttt 2280  
 gtaaaaaaaa aaaaaaa 2297

<210> 58  
 <211> 378  
 <212> PRT  
 <213> Homo sapiens

<400> 58  
 Met Ala Val Ile Gly Leu Pro Tyr Tyr Leu Phe Val Trp Glu Asp Tyr  
 1 5 10 15  
 Asp Lys Tyr Val Ile Phe Ala Ser Phe Asn Leu Ile Trp Ser Thr Val  
 20 25 30

Ile Leu Glu Leu Trp Lys Arg Gly Cys Ala Asn Met Thr Tyr Arg Trp  
           35                          40                          45  
 Gly Thr Leu Leu Met Lys Arg Lys Phe Glu Glu Pro Arg Pro Gly Phe  
           50                          55                          60  
 His Gly Val Leu Gly Ile Asn Ser Ile Thr Gly Lys Glu Glu Pro Leu  
           65                          70                          75                          80  
 Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile Tyr Leu Val Ser Leu Pro  
                           85                          90                          95  
 Phe Val Cys Leu Cys Leu Tyr Phe Ser Leu Tyr Val Met Met Ile Tyr  
                           100                          105                          110  
 Phe Asp Met Glu Val Trp Ala Leu Gly Leu His Glu Asn Ser Gly Ser  
                           115                          120                          125  
 Glu Trp Thr Ser Val Leu Leu Tyr Val Pro Ser Ile Ile Tyr Ala Ile  
           130                          135                          140  
 Val Ile Glu Ile Met Asn Arg Leu Tyr Arg Tyr Ala Ala Glu Phe Leu  
           145                          150                          155                          160  
 Thr Ser Trp Glu Asn His Arg Leu Glu Ser Ala Tyr Gln Asn His Leu  
                           165                          170                          175  
 Ile Leu Lys Val Leu Val Phe Asn Phe Leu Asn Cys Phe Ala Ser Leu  
                           180                          185                          190  
 Phe Tyr Ile Ala Phe Val Leu Lys Asp Met Lys Leu Leu Arg Gln Ser  
                           195                          200                          205  
 Leu Ala Thr Leu Leu Ile Thr Ser Gln Ile Leu Asn Gln Ile Met Glu  
           210                          215                          220  
 Ser Phe Leu Pro Tyr Trp Leu Gln Arg Lys His Gly Val Gln Val Lys  
           225                          230                          235                          240  
 Arg Lys Val Gln Ala Leu Lys Ala Asp Ile Asp Ala Thr Leu Tyr Glu  
                           245                          250                          255  
 Gln Val Ile Leu Glu Lys Glu Met Gly Thr Tyr Leu Gly Thr Phe Asp  
                           260                          265                          270  
 Asp Tyr Leu Glu Leu Phe Leu Gln Phe Gly Tyr Val Ser Leu Phe Ser  
                           275                          280                          285  
 Cys Val Tyr Pro Leu Ala Ala Ala Phe Ala Val Leu Asn Asn Phe Thr  
                           290                          295                          300  
 Glu Val Asn Ser Asp Ala Leu Lys Met Cys Arg Val Phe Lys Arg Pro  
           305                          310                          315                          320  
 Phe Ser Glu Pro Ser Ala Asn Ile Gly Val Trp Gln Met Ile Phe Cys  
                           325                          330                          335  
 Leu Asp Thr Gly Val Lys Arg Gly Leu Asn Cys Lys Val Met Arg Asn  
                           340                          345                          350

Leu Leu Gly Glu Met Glu Met Ser Cys Val Leu Phe Val Val Val Val  
 355 360 365

Val Ser Gln Val Asn Thr Pro Ile Lys Arg  
 370 375

<210> 59  
 <211> 4145  
 <212> DNA  
 <213> Homo sapiens

<400> 59

```

aggctctagaa ttcaagatga agtaaagaag gaaagagagg gtctggagaa tgacttgaaa 60
tctgtgaatt ttgacatgac aagcaagttt ttgacagccc tggctcaaga tgggtgtgata 120
aatgaagaag ctctttctgt tactgaacta gatcgagtct atggaggtct tacaactaaa 180
gtccaagaat ctctaaagaa acaggaggga cttcttaaaa atattcaggt ctcacatcag 240
gaattttcaa aaatgaaaca atctaataat gaagctaact taagagaaga agttttgaag 300
aatttagcta ctgcatatga caactttgtt gaactttagt ctaatttgaa ggaaggcaca 360
aagttttaca atgagttgac tgaaatcctg gtcagggtcc agaacaaatg cagtgtatata 420
gtttttgcac ggaagacaga aagagatgaa ctcttaaagg acttgcaaca aagcattgcc 480
agagaacctt gtgtccttc aattcctaca cctgcgtatc agtcctcacc agcaggagga 540
catgcaccaa ctctccaac tccagcgcca agaaccatgc cgcctactaa gccccagccc 600
ccagccaggc ctccaccacc tgtgcttcca gcaaactgag ctcttctgc tactgtctca 660
tctccagtgg gggctgggac tggctgcccc gctccatcac aaacgcctgg ctacgtcct 720
cctccacagg cgcagggacc accctatccc acctatccag gatatacctgg gtattgccaa 780
atgcccatgc ccatgggcta taatccttat gcgtatggcc agtataatat gccatatcca 840
ccagtgtatc accagagtcc tggacaggct ccatacccgg gacccagca gccttcatac 900
cccttccctc agccccaca gcagtcttac tatccacagc agtaatatgt ctgctcagca 960
gtcagctga ttcagatcag agggaaagaa ataccaaccc tgcaataagt gtactaaact 1020
ctacgctctg gttaatgtaa tgtactctcc tggactgaat gcagtgtata atttctgtct 1080
acagctagaa gctgtgcccc agttccacat ttgattacac atgtgagatt tggctgtgtt 1140
gcagtataaa cactaggtat aataggattt gaaattgcat tacagttcat aaaaattgaa 1200
aatgagaat taaacctgca agtgaaacat ttgaaacgat tatacttttc tacataagac 1260
atggttggga catcagatac ttacaaagat ggtttaagta tggatactag agaaaattaa 1320
gttttcttct tctttggttt attgatttgg tttaatttcc attatgctat ttgcatat 1380
caaggcactg taaatcttat aattttaaaa taaattactt aagaacagtt gtcattgtta 1440
tgttttgtta ttgattctca ttactgtcta atttttttct tggatttagt ctcattttgt 1500
atgtatataa gttaaacaga tactgttttt aagtgcagta atagtacaag ttattatcaa 1560
ggatgtttta cagggaaatc aaaagaatat tatcatactt tatctttcgt atgctgatta 1620
gtaaacgatt tttagacatt attttagaaa gtccataat gtggaagaaa caaacagttg 1680
ctaccaagaa ttcttcaaat aaacatacaa ataaatgtgt atatttaatg ttttattgtt 1740
agcttctcca gaaaattgat gcaaattctg gtaataattc ttgcattttt tccccataac 1800
ctggttaaaa taaatacgcc attggcaata cttcataatg taatggaatt gtttggggaa 1860
cacttactgt accctctcat ctttttcca cttactgtg ttaacttagt gacatttaat 1920
gcccaatatg tatgaataga tctaagccat ttaatttttt ttccttaaaa gattggagta 1980
ttttataatt caaggagcat acaaaacaat ggttgggaac atatgccaat tatggaatag 2040
gctatgtatt taatattaat ctctgccatt aggatatcta ctactgtat aaacctcagt 2100
aaaaatagtg aagacatgca tcatggaatg agaaaatgag aaaggaatga gttgtctaac 2160
atcacagtgg gatctgtttt ttgtgaggtt catttctgaa cacattaggc atatgagcag 2220
atttccagtg aatctattta tgtttatttt ctgagtttca acgctgacct tttcttgcac 2280
tattgtttca ttttaatgat agtgttactt gtcccactgt tgttttcatt gagtttggat 2340
ttatatttta atgttcgaat gaaagtatga ttgtaaaagg gagtgaattg gtttaaaaat 2400
atatgtatat tttaaacttt gttgtgtgta ggaaacatga aggcagtgtta attcaatata 2460
aatgaccttt gatttcatgg aatattaaag ttggtttaaa gtccaatagt taaaccttag 2520
caaaaatagc tttttacttc atcagttgct aagatttaat accttggatt catcaaagt 2580
tgacatgggc ttgtttgact ttctgtaagt ggcatttaag ttccacatc ttattacttg 2640
agggtactta tactaacata agacagttag agttagaggt attacaagtt gctagtttat 2700
aatgtcttac taatgcagaa acaaggaaaa aagcaaaatt ggctgaata ttctcttggg 2760
gaaagagggc accaaagaaa agggtaagt catctgaggg ccaaaagaga tgtataagcc 2820

```

```

ttttagccca ttccecatgc tgggcctgct cacagagcca caggaagatc attcagaaac 2880
taggaaaagga ggccccacaca gctgatcctg ccacagcaca cctgactcac tcggctctgt 2940
tagtgtaacc ttttaaattgt agcaacacaa accctttccc tcttgctcagt tcactcatcc 3000
tttggtttct ttttaatcac ctgtgtctgg gcacagacaa tcacaataaa tgcagccctt 3060
tattactggt aaggatcata ctgttggttt ggagttggaa ggttactact ctgtgattca 3120
ggtgtgtgtt acccatattt ataattaggt tttattatct tcctaaatca aggaaaggaa 3180
atcatcccca gaccatttat gctgagcttt ggaatactat tttaaactgg attgtactta 3240
aataatgaag ctctgcatag aggaactagt cagaagtggg gaaaacactg tctaattttt 3300
atcagctctg tataaagtat tgatctaaga gaactctccc tgtgcccctt ggtctttatt 3360
ctcaattaag aaaaacagtc acatgtcacg acaaaccaat caatctttat gagatattcc 3420
tgtatccata ccccgacttg tttgcaattt ataaacctcc ctttcaaaac taaggagtgtg 3480
cagaaaaaaa tggatttcac agagccttgt gtccctaaag ttctgtccca gtcagcagtc 3540
tttatagttc aaacagatta taaaaaatgt tttccatttg aactttacag tttgcaaaag 3600
tgcttttata cattttctaa tttcagaaac aggataattt gttaagtggg tttcagtttg 3660
ctaataggga ttttttgtgt tttgtttttt aattttcagc atctcttgaa gaatcttgct 3720
acagccaaat ggcattctac tttttaaaga cgtttgcaat tattagtgtg ttcacagtac 3780
agaacaaggt ataaaggaaa aaacctgct aggtagtgtt ataattgcta gattaaaaat 3840
agactagaac aggttcattt taagatttac ttggaagagc aaagaaggaa aaatttatatt 3900
tttaagaaa gagaatattc aggttttatt tctggtatga agtttatatt ttttaaaaaa 3960
atcctatatt atcacaccag agattttaga ttcttttctg gttagaaaca ttgctggtag 4020
ttggattata tttttattgt attcatttat cttaggggga acattgtaaa gaaacaaaaa 4080
gggccagatg aatgtatgct agaaataaaa gttgaaagat tcttacttca aaaaaaaaaa 4140
aaaaa
4145

```

&lt;210&gt; 60

&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 60

```

Met Thr Ser Lys Phe Leu Thr Ala Leu Ala Gln Asp Gly Val Ile Asn
 1             5             10            15

Glu Glu Ala Leu Ser Val Thr Glu Leu Asp Arg Val Tyr Gly Gly Leu
      20             25             30

Thr Thr Lys Val Gln Glu Ser Leu Lys Lys Gln Glu Gly Leu Leu Lys
 35             40             45

Asn Ile Gln Val Ser His Gln Glu Phe Ser Lys Met Lys Gln Ser Asn
 50             55             60

Asn Glu Ala Asn Leu Arg Glu Glu Val Leu Lys Asn Leu Ala Thr Ala
 65             70             75             80

Tyr Asp Asn Phe Val Glu Leu Val Ala Asn Leu Lys Glu Gly Thr Lys
      85             90             95

Phe Tyr Asn Glu Leu Thr Glu Ile Leu Val Arg Phe Gln Asn Lys Cys
 100            105            110

Ser Asp Ile Val Phe Ala Arg Lys Thr Glu Arg Asp Glu Leu Leu Lys
 115            120            125

Asp Leu Gln Gln Ser Ile Ala Arg Glu Pro Ser Ala Pro Ser Ile Pro
 130            135            140

Thr Pro Ala Tyr Gln Ser Ser Pro Ala Gly Gly His Ala Pro Thr Pro
 145            150            155            160

```

Pro Thr Pro Ala Pro Arg Thr Met Pro Pro Thr Lys Pro Gln Pro Pro  
 165 170 175  
 Ala Arg Pro Pro Pro Pro Val Leu Pro Ala Asn Arg Ala Pro Ser Ala  
 180 185 190  
 Thr Ala Pro Ser Pro Val Gly Ala Gly Thr Ala Ala Pro Ala Pro Ser  
 195 200 205  
 Gln Thr Pro Gly Ser Ala Pro Pro Pro Gln Ala Gln Gly Pro Pro Tyr  
 210 215 220  
 Pro Thr Tyr Pro Gly Tyr Pro Gly Tyr Cys Gln Met Pro Met Pro Met  
 225 230 235 240  
 Gly Tyr Asn Pro Tyr Ala Tyr Gly Gln Tyr Asn Met Pro Tyr Pro Pro  
 245 250 255  
 Val Tyr His Gln Ser Pro Gly Gln Ala Pro Tyr Pro Gly Pro Gln Gln  
 260 265 270  
 Pro Ser Tyr Pro Phe Pro Gln Pro Pro Gln Gln Ser Tyr Tyr Pro Gln  
 275 280 285

Gln

<210> 61  
 <211> 1417  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 61

ggtgccccgac atggcgagtg tagtgctgcc gagcggatcc cagtgtgcgg cggcagcggc 60  
 ggcggcgggc cctcccgggc tccggctccg gcttctgctg ttgctcttct ccgcccgggc 120  
 actgatcccc acaggtgatg ggcagaatct gtttacgaaa gacgtgacag tgatcgaggg 180  
 agagggtgcg accatcagtt gccaaagtcaa taagagtgcg gactctgtga ttcagctact 240  
 gaatcccaac aggcagacca tttatttcag ggacttcagg cctttgaagg acagcaggtt 300  
 tcagttgctg aatttttcta gcagtgaact caaagtatca ttgacaaacg tctcaatttc 360  
 tgatgaagga agatactttt gccagctcta taccgatccc ccacaggaaa gttacaccac 420  
 catcacagtc ctggtcccac cacgtaatct gatgatcgat atccagaaag acactgcggt 480  
 ggaaggtgag gagattgaag tcaactgcac tgctatggcc agcaagccag ccacgactat 540  
 caggtgggtc aaagggaaca cagagctaaa aggcaaatcg gaggtggaag agtggtcaga 600  
 catgtacact gtgaccagtc agctgatgct gaaggtgcac aaggaggacg atgggggtccc 660  
 agtgatctgc caggtggagc accctgcggt cactggaaac ctgcagaccc agcggtatct 720  
 agaagtacag tataagcctc aagtgcacat tcagatgact tatcctctac aaggcttaac 780  
 ccgggaaggg gacgcgcttg agttaacatg tgaagccatc gggaagcccc agcctgtgat 840  
 ggtaacttgg gtgagagtcg atgatgaaat gcctcaacac gccgtactgt ctgggcccac 900  
 cctgttcac aataacctaa acaaaacaga taatggtaca taccgctgtg aagcttcaaa 960  
 catagtgggg aaagctcact cggattatat gctgtatgta tacgattccc gagcaggtga 1020  
 agaaggtcgc atcagggcag tggatcatgc cgtgatcggt ggcgtcgtgg cgggtggtgg 1080  
 gttcgccatg ctgtgcttgc tcatcattct ggggcgctat tttgccagac ataaaggtag 1140  
 atacttcact catgaagcca aaggagccga tgacgcagca gacgcagaca cagctataat 1200  
 caatgcagaa ggaggacaga acaactccga agaaaagaaa gactacttca tctagatcag 1260  
 cctttttgtt tcaatgaggt gtccaactgg ccctatttag atgataaaga gacagtgata 1320  
 ttggaacttg cgagaaattc gtgtgttttt ttatgaatgg gtggaaagggt gtgagactgg 1380  
 gaaggcttgg gatttgctgt gtaaaaaaaa aaaaaaa 1417

&lt;210&gt; 62

&lt;211&gt; 414

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 62

Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys Ala Ala Ala Ala  
 1 5 10 15

Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu Leu  
 20 25 30

Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe  
 35 40 45

Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys  
 50 55 60

Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn  
 65 70 75 80

Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg  
 85 90 95

Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr  
 100 105 110

Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr  
 115 120 125

Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro  
 130 135 140

Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu  
 145 150 155 160

Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr  
 165 170 175

Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val  
 180 185 190

Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys  
 195 200 205

Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His  
 210 215 220

Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln  
 225 230 235 240

Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu  
 245 250 255

Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys  
 260 265 270

Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro  
 275 280 285

Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn

290                      295                      300  
 Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly  
 305                      310                      315                      320  
 Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Ser Arg Ala Gly  
 325                      330                      335  
 Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val  
 340                      345                      350  
 Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly  
 355                      360                      365  
 Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys  
 370                      375                      380  
 Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
 385                      390                      395                      400  
 Gly Gly Gln Asn Asn Ser Glu Glu Lys Lys Glu Tyr Phe Ile  
 405                      410

<210> 63  
 <211> 1571  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
 ggccgaggag actgcgaccc tctctctctca gtctgcctta ctaccatgcc gctctacgag 60  
 ggcctgggga gggggggga gaagacggcg gtcgtgatcg acctgggaga ggcctttacc 120  
 aagtgtggat ttgctggaga aactgggtcca agatgtataa ttcctagtgt gataaaaaga 180  
 gctgggatgc ctaagcctgt cagagtgtgt cagtataata tcaatacaga agaattatat 240  
 tcttacctaa aggaattcat ccacatacta tatttcaggc atctattggt gaatcccaga 300  
 gaccgcccag ttgtgattat cgaatcggta ttatgtcctt ctacttcag agagacactc 360  
 actcgtgttc ttttcaaata ttttgagggt ccatctgtct tgcttgctcc aagtcattcta 420  
 atggctcttc tgacgcttgg aattaattct gccatggtcc tagattgtgg atatagggaa 480  
 agcctgggtg taccatata tgaaggaatc ccagtcttaa attgttgggg agcactaccc 540  
 ctaggaggaa aagctcttca caaagagttg gaaactcaac tattggaaca atgtactgtt 600  
 gacacaagtg ttgctaaaga acagagcctt ccctcagtga tgggttcagt tccggaaggt 660  
 gtcttagagg acattaaagc gcgtacttgc tttgtaagtg atctgaagcg aggactaaaa 720  
 atccaagcag caaaatttaa tattgatggg aataatgagc gtccctcccc acccccaaat 780  
 gttgactatc cattagatgg agagaagatt ttacatatcc ttggatcaat cagagattca 840  
 gttgtggaaa ttctttttga acaagataat gaagagcaat cagttgccac tttaatattg 900  
 gattccctta tacagtgtcc gatagacacc aggaagcaac tagcagagaa ttgggtagtc 960  
 ataggtggca ctcttatgtt gccaggattt ctccacagat tgcttgacaga aataaggtat 1020  
 ttggtagaaa aaccaaaata taaaaaagca ctgggacta agacatttcg aattcatact 1080  
 ccacctgcaa aagctaattg tgtggcctgg ttgggagggg ctatttttgg agcattacaa 1140  
 gatatacttg ggagccgttc tgtttcaaag gaatattata atcagacggg ccgtatacct 1200  
 gattgggtgt ctctcaataa ccacaccttg gaaatgatgt ttgatgtcgg gaaaactcaa 1260  
 ccacctctga tgaagagagc attttccact gagaaataga agtttgatta aaaatcaacc 1320  
 ttgcttcata tcaaatattt aaccaattat aagcaaattg tacaaagtat gtaggatgtt 1380  
 ttgttataga ggactatagt ggaagtgaat gcattctgtg tttactcttt gcattaatat 1440  
 ataattcttt tgactttgtt tctcttgtgt agtggtaaaa tggtagctgg tgcttattga 1500  
 gatttgctgt atttatatca ataaagtata gtaaaagcaa aaaaaaaaaa aaaaaaaaaa 1560  
 aaaaaaaaaa a  
 1571

<210> 64  
 <211> 417

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 64

Met Pro Leu Tyr Glu Gly Leu Gly Ser Gly Gly Glu Lys Thr Ala Val  
 1 5 10 15

Val Ile Asp Leu Gly Glu Ala Phe Thr Lys Cys Gly Phe Ala Gly Glu  
 20 25 30

Thr Gly Pro Arg Cys Ile Ile Pro Ser Val Ile Lys Arg Ala Gly Met  
 35 40 45

Pro Lys Pro Val Arg Val Val Gln Tyr Asn Ile Asn Thr Glu Glu Leu  
 50 55 60

Tyr Ser Tyr Leu Lys Glu Phe Ile His Ile Leu Tyr Phe Arg His Leu  
 65 70 75 80

Leu Val Asn Pro Arg Asp Arg Arg Val Val Ile Ile Glu Ser Val Leu  
 85 90 95

Cys Pro Ser His Phe Arg Glu Thr Leu Thr Arg Val Leu Phe Lys Tyr  
 100 105 110

Phe Glu Val Pro Ser Val Leu Leu Ala Pro Ser His Leu Met Ala Leu  
 115 120 125

Leu Thr Leu Gly Ile Asn Ser Ala Met Val Leu Asp Cys Gly Tyr Arg  
 130 135 140

Glu Ser Leu Val Leu Pro Ile Tyr Glu Gly Ile Pro Val Leu Asn Cys  
 145 150 155 160

Trp Gly Ala Leu Pro Leu Gly Gly Lys Ala Leu His Lys Glu Leu Glu  
 165 170 175

Thr Gln Leu Leu Glu Gln Cys Thr Val Asp Thr Ser Val Ala Lys Glu  
 180 185 190

Gln Ser Leu Pro Ser Val Met Gly Ser Val Pro Glu Gly Val Leu Glu  
 195 200 205

Asp Ile Lys Ala Arg Thr Cys Phe Val Ser Asp Leu Lys Arg Gly Leu  
 210 215 220

Lys Ile Gln Ala Ala Lys Phe Asn Ile Asp Gly Asn Asn Glu Arg Pro  
 225 230 235 240

Ser Pro Pro Pro Asn Val Asp Tyr Pro Leu Asp Gly Glu Lys Ile Leu  
 245 250 255

His Ile Leu Gly Ser Ile Arg Asp Ser Val Val Glu Ile Leu Phe Glu  
 260 265 270

Gln Asp Asn Glu Glu Gln Ser Val Ala Thr Leu Ile Leu Asp Ser Leu  
 275 280 285

Ile Gln Cys Pro Ile Asp Thr Arg Lys Gln Leu Ala Glu Asn Leu Val  
 290 295 300



Val Ile Gly Gly Thr Ser Met Leu Pro Gly Phe Leu His Arg Leu Leu  
 305 310 315 320

Ala Glu Ile Arg Tyr Leu Val Glu Lys Pro Lys Tyr Lys Lys Ala Leu  
 325 330 335

Gly Thr Lys Thr Phe Arg Ile His Thr Pro Pro Ala Lys Ala Asn Cys  
 340 345 350

Val Ala Trp Leu Gly Gly Ala Ile Phe Gly Ala Leu Gln Asp Ile Leu  
 355 360 365

Gly Ser Arg Ser Val Ser Lys Glu Tyr Tyr Asn Gln Thr Gly Arg Ile  
 370 375 380

Pro Asp Trp Cys Ser Leu Asn Asn Pro Pro Leu Glu Met Met Phe Asp  
 385 390 395 400

Val Gly Lys Thr Gln Pro Pro Leu Met Lys Arg Ala Phe Ser Thr Glu  
 405 410 415

Lys

&lt;210&gt; 65

&lt;211&gt; 1752

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 65

ggccaatcag agggacggcc ccagaatggc atggtagatg gaacgcagct gagaggtctg 60  
 acaagatgta ccaggtccca ctaccactgg atcgggatgg gaccctggta cggctccgct 120  
 tcaccatggt ggccctggtc acggtctgct gtccacttgt cgccttctc ttctgcatcc 180  
 tctggtccct gctcttcac ttcaaggaga caacggccac aactgtggg gtgccaatt 240  
 acctgccctc ggtgagctca gccatcggcg gggaggtgcc ccagcgctac gtgtggcggt 300  
 tctgcatcgg cctgcaactc gcgcctcgt tcttgggtggc ctctgcctac tgggaaccact 360  
 acctcagctg cacctccccg tgttctctg atcgcccgct ctgcgcctc aacttcggcc 420  
 tcaatgtcgt ggagaacctc gcgttgctag tgctcaacta tgtctctcc tccgaggact 480  
 tcaccatcca cgaaaatgct ttcatttgtt tcattgcctc atccctcggg cacatgctcc 540  
 tcacctgcat tctctggcgg ttgaccaaga agcacacagt aagtcaggag gatcgcaagt 600  
 cctacagctg gaaacagcgg ctcttcatca tcaacttcat ctctctctc tcggcgctgg 660  
 ctgtctactt tcggcacaac atgtattgtg aggctggagt gtacaccatc tttgccatcc 720  
 tggagtacac tgttgtctta accaaccatg cgttccacat gacggcctgg tgggacttcg 780  
 ggaacaagga gctgctcata acctctcagc ctgaggaaaa gcgattctga acccttcagt 840  
 cctgcttggg aggacgcagc ccactgcccc gaaacaagaa acacgatacc attctggcct 900  
 tccccacccc acatcctctc ttggccttac tgaagatggg ggaagggtaa gaaggagg 960  
 tgtaggccaa ggctcacccc agtgctgctg gcttctctc tccaccctc atatggcggt 1020  
 ggggtcctca aacatcacct ttacctgaga ggccccaaga agctgagctg gcagagagct 1080  
 ccaccatttg gtgctaaaaa aaaaaacgtc ctgaggttca tgaccaccat ccagtttctg 1140  
 gcctttacac agtcacctt cactgaggtc aggagccct gagcagtggc tgctccctga 1200  
 caaccacagc ctttctctg cacgggggtc attcatagga ctaatgtatt tcatgatcta 1260  
 ctgtgcacat ccaggcctgt ggccacagtc ccttgctaaa gttgctcagg tgttctagtc 1320  
 ctgacttcac ctttttgatt tgggtgtgtg cctagggtat gtacccttcc ccatctgagc 1380  
 ctcggtgtgt ccatgtgtct ggcgggggat ggggtggactg tatgatttcc aaggactcta 1440  
 ccagtcaagt gttctgatgt catcgggtgg aggtggtgt ctatacctaa aggatgacct 1500  
 gctccagaaa cagcaccagc acagcatgta ttttctctc ttctgaaagt tctggcttgt 1560  
 agaccctctc cctcctttgc aaaggtatgg gatagagggg tcagatgcag atctctactg 1620  
 taaaatgggc tccctgggtat ctctgtctt ccctactgct ccaaacccta aattttgggt 1680

gtacatttta ttgaaagga aaataaattt ttttttggg ccaaaaaaaaaa aaaaaaaaaa 1740  
 aaaaaaaaaa aa 1752

<210> 66  
 <211> 254  
 <212> PRT  
 <213> Homo sapiens

<400> 66  
 Met Tyr Gln Val Pro Leu Pro Leu Asp Arg Asp Gly Thr Leu Val Arg  
 1 5 10 15  
 Leu Arg Phe Thr Met Val Ala Leu Val Thr Val Cys Cys Pro Leu Val  
 20 25 30  
 Ala Phe Leu Phe Cys Ile Leu Trp Ser Leu Leu Phe His Phe Lys Glu  
 35 40 45  
 Thr Thr Ala Thr His Cys Gly Val Pro Asn Tyr Leu Pro Ser Val Ser  
 50 55 60  
 Ser Ala Ile Gly Gly Glu Val Pro Gln Arg Tyr Val Trp Arg Phe Cys  
 65 70 75 80  
 Ile Gly Leu His Ser Ala Pro Arg Phe Leu Val Ala Phe Ala Tyr Trp  
 85 90 95  
 Asn His Tyr Leu Ser Cys Thr Ser Pro Cys Ser Cys Tyr Arg Pro Leu  
 100 105 110  
 Cys Arg Leu Asn Phe Gly Leu Asn Val Val Glu Asn Leu Ala Leu Leu  
 115 120 125  
 Val Leu Thr Tyr Val Ser Ser Ser Glu Asp Phe Thr Ile His Glu Asn  
 130 135 140  
 Ala Phe Ile Val Phe Ile Ala Ser Ser Leu Gly His Met Leu Leu Thr  
 145 150 155 160  
 Cys Ile Leu Trp Arg Leu Thr Lys Lys His Thr Val Ser Gln Glu Asp  
 165 170 175  
 Arg Lys Ser Tyr Ser Trp Lys Gln Arg Leu Phe Ile Ile Asn Phe Ile  
 180 185 190  
 Ser Phe Phe Ser Ala Leu Ala Val Tyr Phe Arg His Asn Met Tyr Cys  
 195 200 205  
 Glu Ala Gly Val Tyr Thr Ile Phe Ala Ile Leu Glu Tyr Thr Val Val  
 210 215 220  
 Leu Thr Asn Met Ala Phe His Met Thr Ala Trp Trp Asp Phe Gly Asn  
 225 230 235 240  
 Lys Glu Leu Leu Ile Thr Ser Gln Pro Glu Glu Lys Arg Phe  
 245 250

<210> 67  
 <211> 781

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 67

```

cactcctgca gacaaggcac tgattgcccc agaccatgta gttccagctc cagaagagtg 60
ctatgtgtat agtccattgg gctctgctta taaacttcaa agttacactg aaggatacgg 120
taaaaacacc agtttagtaa ccatttttat gatttggaat accatgatgg gaacatctat 180
actaagcatt ccttggggca taaaacaggc tggatttact actggaatgt gtgtcatcat 240
actgatgggc cttttaacac tttattgctg ctacagagta gtgaaatcac ggactatgat 300
gttttcattg gataaccacta cctgggaata tccagatgtc tgcagacatt atttcggctc 360
ctttgggcag tggtcgagtc tcctcttctc cttggtgtct ctcattggag caatgatagt 420
ttattgggtg cttatgtcaa attttctttt taatactgga aagtttattt ttagtaagta 480
tctatatcat atgcttttaa cacagtactt tcaaatacta ttaccactgt aatgttagtt 540
ctagccttaa attctaggac ttgggataaa taaaataaga agtaacatat ataattttgg 600
aaaatatatt ttattcagtt ggctttctgt ggttggtgctc tcaaatatag tgtatgctta 660
tttccaaaca ttaatctttg aaggaataat attcctccaa aatctttagt taaaataaaa 720
tatgtctata atccaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 780
a

```

781

&lt;210&gt; 68

&lt;211&gt; 127

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 68

```

Met Ile Trp Asn Thr Met Met Gly Thr Ser Ile Leu Ser Ile Pro Trp
  1                      5                      10                      15

Gly Ile Lys Gln Ala Gly Phe Thr Thr Gly Met Cys Val Ile Ile Leu
          20                      25                      30

Met Gly Leu Leu Thr Leu Tyr Cys Cys Tyr Arg Val Val Lys Ser Arg
          35                      40                      45

Thr Met Met Phe Ser Leu Asp Thr Thr Thr Trp Glu Tyr Pro Asp Val
          50                      55                      60

Cys Arg His Tyr Phe Gly Ser Phe Gly Gln Trp Ser Ser Leu Leu Phe
          65                      70                      75                      80

Ser Leu Val Ser Leu Ile Gly Ala Met Ile Val Tyr Trp Val Leu Met
          85                      90                      95

Ser Asn Phe Leu Phe Asn Thr Gly Lys Phe Ile Phe Ser Lys Tyr Leu
          100                     105                     110

Tyr His Met Leu Leu Thr Gln Tyr Phe Gln Ile Leu Leu Pro Leu
          115                     120                     125

```

&lt;210&gt; 69

&lt;211&gt; 649

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 69

```

gagcaactcc cttcccatc tctgctcacc atgtggagcg tgaaatcgct cctggctcctg 60
cttctgtgcc tcacctgcag ctatgccttt atgttctctt ctctgagaca gaaaactagc 120
gaaccccgagg ggaagggtgca atacggagag cactttcgga ttcggcagaa tctaccagag 180
cacacccaag gctggcttgg gagcaaatgg ctctggcttc tttttgttgt tgtgccgttt 240

```

```

gtgatactgc agtgtcaaag agacagttag aagaataagg agcagagtcc tcctggcctt 300
cgaggcggcc aacttcactc tccattaaag aaaaaaagaa atgcttcccc caacaaagac 360
tgtgcattca ataccttaat ggaactcgag gtggagctta tgaaatttgt gtccaaagtg 420
cggaatctta aacgtgccat ggcaacaggt agtggcagta acctcaggct tcgaaagtca 480
gagatgcctg cagatccata ccatgtcacg atctgtgaaa tatggggaga agaaagctct 540
agctgaatgg atttgtgtgt caggagagaa aaaagttgag tgttgacaaa ctgtatgcaa 600
actaataaaa ctattctgaa gaaaagaaaa aaaaaaaaaa aaaaaaaaaa 649

```

&lt;210&gt; 70

&lt;211&gt; 171

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 70

```

Met Trp Thr Leu Lys Ser Ser Leu Val Leu Leu Leu Cys Leu Thr Cys
  1                      5                      10                      15

Ser Tyr Ala Phe Met Phe Ser Ser Leu Arg Gln Lys Thr Ser Glu Pro
          20                      25                      30

Gln Gly Lys Val Gln Tyr Gly Glu His Phe Arg Ile Arg Gln Asn Leu
      35                      40                      45

Pro Glu His Thr Gln Gly Trp Leu Gly Ser Lys Trp Leu Trp Leu Leu
      50                      55                      60

Phe Val Val Val Pro Phe Val Ile Leu Gln Cys Gln Arg Asp Ser Glu
      65                      70                      75                      80

Lys Asn Lys Glu Gln Ser Pro Pro Gly Leu Arg Gly Gly Gln Leu His
          85                      90                      95

Ser Pro Leu Lys Lys Lys Arg Asn Ala Ser Pro Asn Lys Asp Cys Ala
          100                      105                      110

Phe Asn Thr Leu Met Glu Leu Glu Val Glu Leu Met Lys Phe Val Ser
          115                      120                      125

Lys Val Arg Asn Leu Lys Arg Ala Met Ala Thr Gly Ser Gly Ser Asn
          130                      135                      140

Leu Arg Leu Arg Lys Ser Glu Met Pro Ala Asp Pro Tyr His Val Thr
          145                      150                      155                      160

Ile Cys Glu Ile Trp Gly Glu Glu Ser Ser Ser
          165                      170

```

&lt;210&gt; 71

&lt;211&gt; 1456

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 71

```

cagggtctgc ttatctgcaa gtgcagagag gcctctgctt cagctggggc acccatcctg 60
tcgggcactt gtctcaccgt ggatgggtcat catcataaaa atgaggagag ctggcacgat 120
gggtgccggg aatgctactg tctcaatgga cgggaaatgt gtgccctgat cacctgcccg 180
gtgcctgcct gtggcaaccc caccattcac cctggacagt gctgcccacg atgtgcagat 240
gactttgtgg tgcagaagcc agagctcagt actccctcca ttgcccacgc ccctggagga 300
gaatactttg tggaaggaga aacgtggaac attgactcct gtactcagtg cacctgccac 360

```

```

agcggacggg tgctgtgtga gacagaggtg tgcccaccgc tgctctgcca gaaccctca 420
cgaccccagg attcctgctg cccacagtgt acagatcaac cttttcgcc ttcctgtgcc 480
cgcaataaca gcgtaccta ttattgcaaa aatgatgaag gggatatatt cctggcagct 540
gagtcctgga agcctgacgt ttgtaccagc tgcactgca ttgatagcgt aattagctgt 600
ttctctgagt cctgcccttc tgtatcctgt gaaagacctg tcttgagaaa aggccagtgt 660
tgccctact gcatagaaga cacaattcca aagaagggtg tgtgccactt cagtgggaag 720
gcctatgccg acgaggagcg gtgggacctt gacagctgca cccactgcta ctgcctgcag 780
ggccagaccc tctgctcgac cgtcagctgc cccctctgc cctgtgttga gcccatacaac 840
gtggaaggaa gttgctgcc aatgtgtcca gaaatgtatg tcccagaacc aaccaatata 900
cccattgaga agacaaacca tgcaggagag gttgacctgg aggttcccct gtggccacg 960
cctagtga aa atgatatcgt ccatctccct agagatatgg gtcacctcca ggtagattac 1020
agagataaca ggctgcacc aagtgaagat tcttactgg actccattgc ctcagttgtg 1080
gttcccataa ttatatgctt ctctattata atagcattcc tattcatcaa tcagaagaaa 1140
cagtggatac cactgctttg ctggtatcga acaccaacta agccttcttc cttaaataat 1200
cagctagtat ctgtggactg caagaaagga accagagtcc aggtggacag tcccagaga 1260
atgctaagaa ttgcagaacc agatgcaaga ttcagtggct tctacagcat gcaaaaacag 1320
aaccatctac aggcagacaa tttctacaa acagtgtgaa gaaaggcaac taggatgagg 1380
tttcaaaaga cggaagacga ctaaactctg tctaaaaagt aaactagaat ttgtgcactt 1440
aaaaaaaaa aaaaaa 1456

```

&lt;210&gt; 72

&lt;211&gt; 400

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

```

Met Cys Ala Leu Ile Thr Cys Pro Val Pro Ala Cys Gly Asn Pro Thr
  1             5             10             15

Ile His Pro Gly Gln Cys Cys Pro Ser Cys Ala Asp Asp Phe Val Val
             20             25             30

Gln Lys Pro Glu Leu Ser Thr Pro Ser Ile Cys His Ala Pro Gly Gly
             35             40             45

Glu Tyr Phe Val Glu Gly Glu Thr Trp Asn Ile Asp Ser Cys Thr Gln
             50             55             60

Cys Thr Cys His Ser Gly Arg Val Leu Cys Glu Thr Glu Val Cys Pro
             65             70             75             80

Pro Leu Leu Cys Gln Asn Pro Ser Arg Thr Gln Asp Ser Cys Cys Pro
             85             90             95

Gln Cys Thr Asp Gln Pro Phe Arg Pro Ser Leu Ser Arg Asn Asn Ser
             100            105            110

Val Pro Asn Tyr Cys Lys Asn Asp Glu Gly Asp Ile Phe Leu Ala Ala
             115            120            125

Glu Ser Trp Lys Pro Asp Val Cys Thr Ser Cys Ile Cys Ile Asp Ser
             130            135            140

Val Ile Ser Cys Phe Ser Glu Ser Cys Pro Ser Val Ser Cys Glu Arg
             145            150            155            160

Pro Val Leu Arg Lys Gly Gln Cys Cys Pro Tyr Cys Ile Glu Asp Thr
             165            170            175

Ile Pro Lys Lys Val Val Cys His Phe Ser Gly Lys Ala Tyr Ala Asp

```

180	185	190
Glu Glu Arg Trp Asp Leu Asp Ser Cys Thr His Cys Tyr Cys Leu Gln 195 200 205		
Gly Gln Thr Leu Cys Ser Thr Val Ser Cys Pro Pro Leu Pro Cys Val 210 215 220		
Glu Pro Ile Asn Val Glu Gly Ser Cys Cys Pro Met Cys Pro Glu Met 225 230 235 240		
Tyr Val Pro Glu Pro Thr Asn Ile Pro Ile Glu Lys Thr Asn His Arg 245 250 255		
Gly Glu Val Asp Leu Glu Val Pro Leu Trp Pro Thr Pro Ser Glu Asn 260 265 270		
Asp Ile Val His Leu Pro Arg Asp Met Gly His Leu Gln Val Asp Tyr 275 280 285		
Arg Asp Asn Arg Leu His Pro Ser Glu Asp Ser Ser Leu Asp Ser Ile 290 295 300		
Ala Ser Val Val Val Pro Ile Ile Ile Cys Leu Ser Ile Ile Ile Ala 305 310 315 320		
Phe Leu Phe Ile Asn Gln Lys Lys Gln Trp Ile Pro Leu Leu Cys Trp 325 330 335		
Tyr Arg Thr Pro Thr Lys Pro Ser Ser Leu Asn Asn Gln Leu Val Ser 340 345 350		
Val Asp Cys Lys Lys Gly Thr Arg Val Gln Val Asp Ser Ser Gln Arg 355 360 365		
Met Leu Arg Ile Ala Glu Pro Asp Ala Arg Phe Ser Gly Phe Tyr Ser 370 375 380		
Met Gln Lys Gln Asn His Leu Gln Ala Asp Asn Phe Tyr Gln Thr Val 385 390 395 400		

&lt;210&gt; 73

&lt;211&gt; 4723

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

```

ggccttcatg gcctattttt tttttttttt aaatgataca acttaatttt attaggacaa 60
ggctgggtggg cactggagtg gcaccttcag ggccaggaga ggcactgggg aggggtcaca 120
ggatgctact cgggcaccta gaagccacag ctgccctcca cagagcggca ctgcaccatg 180
cgcaggaatg tctcgacctt gtccatgtcc ttctgaagc agtagagcag cccgtagttc 240
ttgagcagtg cgtcatggtt gtgcgagttt gtgtcaaact tgctgtaggt ctgcttgagg 300
atctgcccag tccggcggct gccgtcttcc agcctcccca tcagcgtttg gatgccttcc 360
tctaggtcct ttaggagggtg atagtcacgt ttgtccgagg tgtcatacac caggttggtg 420
gcgaacatac tcctgaggaa ccgcacgggc tcagccacg actcgatgag cagcagggag 480
atgcggagca gctctagatt ggatttctgt tgcgtttcct ccatgttgga ggggtgcgga 540
atagagtctg agaagcagaa ggaggtcttg gagtcatgca ggaatgaata cttctggtcc 600
tttgggatat aggtttcttc aaactcctgg taggtgtcaa tggccagctg gtgcgcgcga 660
tgggcttgga gcatagcgtg gtcaaaaagc ctggataacg gaacggtttg gacggcacca 720

```

```

gcctcttgaa gccagggcag gcagagcagg gcaaaagcca ggagcaggga cgtccgggag 780
cctggagcca ttgccactag gtgagctgtc cacaggaccc tgagtgggtc ggggagttcg 840
gccttcattgg cctaggagcg gcgcaggagt gaggcgagcg gggcgcgcg agcgagaccc 900
gcggatcttg tgctgcgcca ccgcgccac tcggcagctc gggaggcggg gaccggcccg 960
gaggctgcgc cgctgcgggg ccggccgact cggaggagga gagggaggag gcgcccgcg 1020
ccggggctgg agccgagcgc agcagccacc gccgcgcgc cgcagaagt ttgggttgaa 1080
ccggagctgc cgggaggaaa cttttttctt ttttccccct ccctcccggy aggaggagga 1140
ggaggaggag gggaagctgc cgccggcgcc aaggctcgtg ggctcggggg cggcgcggcc 1200
cgcagaaggg gcgggggcct cgcccccgca ggggaggcgc gccccggggg ccccgagagg 1260
ggcggtgagg acccggggct gctggtgcgg cggcgcgcg gcgcgctgtg ccccgcgag 1320
gggaggggcg ccgccccgct ccgggcccg ctgcgaggag gaggcgcgcg cggcgcgagg 1380
ggatgtactt ggtggcgggg gacagggggt tggccggctg cgggcacctc ctggtctcgc 1440
tgctggggct gctgctgctg ctggcgcgct ccggcaccgg ggcgctggtc tgctgcct 1500
gtgacgagtc caagtgcgag gagcccagga actgcccggg gagcatcgtg caggcgctct 1560
gcggctgctg ctacacgtgc gccagccaga ggaacgagag ctgcgcgcg accctcgga 1620
tttacggaac ctgcgaccgg gggctgcgtt gtgtcatccg ccccccgctc aatggcgact 1680
ccctcaccga gtacgaagcg ggcgtttgcg aagatgagaa ctggactgat gaccaactgc 1740
ttggttttaa accatgcaat gaaaacctta ttgctggctg caatataatc aatgggaaat 1800
gtgaatgtaa caccattcga acctgcagca atccctttga gtttccaagt caggatatgt 1860
gcctttcagc tttaaagaga attgaagaag agaagccaga ttgctccaag gcccgctgtg 1920
aagtccagtt ctctccacgt tgtcctgaag attctgttct gatcgagggt tatgtctctc 1980
ctggggagtg ctgtccctta ccagccgct gcgtgtgcaa ccccgaggc tgtctgcgca 2040
aagtctgcca cgcgggaaac ctgaacatac tattgtcaaa agcctcaggg aagccgggag 2100
agtgtgtgta cctctatgag tgcaaacacc ggttccggct ggactgcagg actgtggaat 2160
gccctcctgt tcagcagacc gcgtgtcccc cggacagcta tgaaactcaa gtcagactaa 2220
ctgcagatgg ttgctgtact ttgccaacaa gatgcgagtg tctctctggc ttatgtgggt 2280
tccccgtgtg tgaggtggga tccactcccc gcatagtctc tcgtggcgat gggacacctg 2340
gaaagtgtgt tgatgtcttt gaatgtgtta atgatacaaa gccagcctgc gtatttaaca 2400
atgtggaata ttatgatgga gacatgtttc gaatggacaa ctgtcggttc tgtcgatgcc 2460
aagggggcgt tgccatctgc ttcactgccc agtgtgggtg gataaactgc gagaggtagt 2520
acgtgccgga aggagagtgc tgcccagtg gtgaagatcc agtgtatcct tttaataatc 2580
ccgctggctg ctatgccaat ggccgtgacc ttgcccacgg agaccggtgg cgggaagacg 2640
actgcacatt ctgccagtgc gtcaacgggtg aacgccactg cgttgcgacc gtctgcggag 2700
agacctgcac aaacctgtg aaagtgcctg gggagtgttg ccctgtgtgc gaagaaccaa 2760
ccatcatcac agttgatcca cctgcatgtg gggagtattc aaactgcact ctgacaggga 2820
aggactgcat taatggtttc aaacgcgac acaatggttg tcggacctgt cagtgcataa 2880
acaccgagga actatgttca gaacgtaaac aaggctgcac ctgaaactgt cccttcgggt 2940
tccttactga tgcccaaaac tgtgagatct gtgagtgcg cccaaggccc aagaagtgc 3000
gaccataat ctgtgacaag tattgtccac ttggattgct gaagaataag cacggctgtg 3060
acatctgtcg ctgtaagaaa tgtccagagc tctcatgcag taagatctgc cccttgggtt 3120
tccagcagga cagtcacggc tgtcttatct gcaagtgcag agaggcctct gcttcagctg 3180
ggccacccat cctgtcgggc acttgtctca ccgtggatgg tcatcatcat aaaaatgagg 3240
agagctggca cgatgggtgc cgggaatgct actgtctcaa tggacgggaa atgtgtgccc 3300
tgatcacctg cccggtgcct gcctgtggca accccacct tcacctgga cagtgtgcc 3360
catcatgtgc agatgacttt gtggtgcaga agccagagct cagtactccc tccatttgcc 3420
acgcccctgg aggagaatac tttgtggaag gagaaactgc gaacattgac tctgtactc 3480
agtgcacctg ccacagcggg cgggtgctgt gtgagacaga ggtgtgccc cgcgtgctct 3540
gccagaacce ctcacgcacc caggattcct gctgcccaca gtgtacagat caaccttttc 3600
ggccttcctt gtcccgaat aacagcgtac ctaattactg caaaaatgat gaaggggata 3660
tattcctggc agctgagtc tggaagcctg acgtttgtac cagctgcac tgcattgata 3720
gcgtaattag ctgtttctct gagtccctgc cttctgtatc ctgtgaaaga cctgtcttga 3780
gaaaaggcca gtgttgtccc tactgcatag aagacacaa tccaaagaag gtggtgtgcc 3840
acttcagtgg gaaggcctat gccgacgagg agcgggtggga ccttgacagc tgcacctact 3900
gctactgcct gcagggccag accctctgct cgaccgtcag ctgccccct ctgccctgtg 3960
ttgagcccat caacgtggaa ggaagtgtgt gcccaatgtg tccagaaatg tatgtcccag 4020
aaccaaccaa tataccattt gagaagacaa accatcgagg agaggttgac ctggaggttc 4080
ccctgtggcc cagcctagt gaaaatgata tcgtccatct ccctagagat atgggtcacc 4140
tccaggtaga ttacagagat aacaggctgc acccaagtga agattcttca ctggactcca 4200
ttgcctcagt tgtggttccc ataattatat gcctctctat tataatagca ttcctattca 4260
tcaatcagaa gaaacagtgg ataccactgc tttgctggta tcgaacacca actaagcctt 4320

```

```

cttccttaaa taatcagtta gtatctgtgg actgcaagaa aggaaccaga gtccaggtgg 4380
acagttccca gagaatgcta agaattgcag aaccagatgc aagattcagt ggcttctaca 4440
gcatgcaaaa acagaaccat ctacaggcag acaatttcta ccaaacagtg tgaagaaagg 4500
caactaggat gaggtttcaa aagacggaag acgactaaat ctgctctaaa aagtaaacta 4560
gaatttgtag acttgcttag tggattgtat tggattgtga cttgatgtac agcgctaaga 4620
ccttactggg atgggctctg tctacagcaa tgtgcagaac aagcattccc cctcaaacct 4680
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 4723

```

<210> 74

<211> 1036

<212> PRT

<213> Homo sapiens

<400> 74

```

Met Tyr Leu Val Ala Gly Asp Arg Gly Leu Ala Gly Cys Gly His Leu
  1             5             10             15

Leu Val Ser Leu Leu Gly Leu Leu Leu Leu Leu Ala Arg Ser Gly Thr
      20             25             30

Arg Ala Leu Val Cys Leu Pro Cys Asp Glu Ser Lys Cys Glu Glu Pro
      35             40             45

Arg Asn Cys Pro Gly Ser Ile Val Gln Gly Val Cys Gly Cys Cys Tyr
      50             55             60

Thr Cys Ala Ser Gln Arg Asn Glu Ser Cys Gly Gly Thr Phe Gly Ile
      65             70             75             80

Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu
      85             90             95

Asn Gly Asp Ser Leu Thr Glu Tyr Glu Ala Gly Val Cys Glu Asp Glu
      100            105            110

Asn Trp Thr Asp Asp Gln Leu Leu Gly Phe Lys Pro Cys Asn Glu Asn
      115            120            125

Leu Ile Ala Gly Cys Asn Ile Ile Asn Gly Lys Cys Glu Cys Asn Thr
      130            135            140

Ile Arg Thr Cys Ser Asn Pro Phe Glu Phe Pro Ser Gln Asp Met Cys
      145            150            155            160

Leu Ser Ala Leu Lys Arg Ile Glu Glu Glu Lys Pro Asp Cys Ser Lys
      165            170            175

Ala Arg Cys Glu Val Gln Phe Ser Pro Arg Cys Pro Glu Asp Ser Val
      180            185            190

Leu Ile Glu Gly Tyr Ala Pro Pro Gly Glu Cys Cys Pro Leu Pro Ser
      195            200            205

Arg Cys Val Cys Asn Pro Ala Gly Cys Leu Arg Lys Val Cys Gln Pro
      210            215            220

Gly Asn Leu Asn Ile Leu Val Ser Lys Ala Ser Gly Lys Pro Gly Glu
      225            230            235            240

Cys Cys Asp Leu Tyr Glu Cys Lys Pro Val Phe Gly Val Asp Cys Arg

```



	245		250		255
Thr Val Glu Cys Pro Pro Val Gln Gln Thr Ala Cys Pro Pro Asp Ser	260		265		270
Tyr Glu Thr Gln Val Arg Leu Thr Ala Asp Gly Cys Cys Thr Leu Pro	275		280		285
Thr Arg Cys Glu Cys Leu Ser Gly Leu Cys Gly Phe Pro Val Cys Glu	290		295		300
Val Gly Ser Thr Pro Arg Ile Val Ser Arg Gly Asp Gly Thr Pro Gly	305		310		315
Lys Cys Cys Asp Val Phe Glu Cys Val Asn Asp Thr Lys Pro Ala Cys	325		330		335
Val Phe Asn Asn Val Glu Tyr Tyr Asp Gly Asp Met Phe Arg Met Asp	340		345		350
Asn Cys Arg Phe Cys Arg Cys Gln Gly Gly Val Ala Ile Cys Phe Thr	355		360		365
Ala Gln Cys Gly Glu Ile Asn Cys Glu Arg Tyr Tyr Val Pro Glu Gly	370		375		380
Glu Cys Cys Pro Val Cys Glu Asp Pro Val Tyr Pro Phe Asn Asn Pro	385		390		395
Ala Gly Cys Tyr Ala Asn Gly Leu Ile Leu Ala His Gly Asp Arg Trp	405		410		415
Arg Glu Asp Asp Cys Thr Phe Cys Gln Cys Val Asn Gly Glu Arg His	420		425		430
Cys Val Ala Thr Val Cys Gly Gln Thr Cys Thr Asn Pro Val Lys Val	435		440		445
Pro Gly Glu Cys Cys Pro Val Cys Glu Glu Pro Thr Ile Ile Thr Val	450		455		460
Asp Pro Pro Ala Cys Gly Glu Leu Ser Asn Cys Thr Leu Thr Gly Lys	465		470		475
Asp Cys Ile Asn Gly Phe Lys Arg Asp His Asn Gly Cys Arg Thr Cys	485		490		495
Gln Cys Ile Asn Thr Glu Glu Leu Cys Ser Glu Arg Lys Gln Gly Cys	500		505		510
Thr Leu Asn Cys Pro Phe Gly Phe Leu Thr Asp Ala Gln Asn Cys Glu	515		520		525
Ile Cys Glu Cys Arg Pro Arg Pro Lys Lys Cys Arg Pro Ile Ile Cys	530		535		540
Asp Lys Tyr Cys Pro Leu Gly Leu Leu Lys Asn Lys His Gly Cys Asp	545		550		555
Ile Cys Arg Cys Lys Lys Cys Pro Glu Leu Ser Cys Ser Lys Ile Cys					560

565										570					575									
Pro	Leu	Gly	Phe	Gln	Gln	Asp	Ser	His	Gly	Cys	Leu	Ile	Cys	Lys	Cys									
580										585					590									
Arg	Glu	Ala	Ser	Ala	Ser	Ala	Gly	Pro	Pro	Ile	Leu	Ser	Gly	Thr	Cys									
595										600					605									
Leu	Thr	Val	Asp	Gly	His	His	His	Lys	Asn	Glu	Glu	Ser	Trp	His	Asp									
610										615					620									
Gly	Cys	Arg	Glu	Cys	Tyr	Cys	Leu	Asn	Gly	Arg	Glu	Met	Cys	Ala	Leu									
625										630					635					640				
Ile	Thr	Cys	Pro	Val	Pro	Ala	Cys	Gly	Asn	Pro	Thr	Ile	His	Pro	Gly									
645										650					655									
Gln	Cys	Cys	Pro	Ser	Cys	Ala	Asp	Asp	Phe	Val	Val	Gln	Lys	Pro	Glu									
660										665					670									
Leu	Ser	Thr	Pro	Ser	Ile	Cys	His	Ala	Pro	Gly	Gly	Glu	Tyr	Phe	Val									
675										680					685									
Glu	Gly	Glu	Thr	Trp	Asn	Ile	Asp	Ser	Cys	Thr	Gln	Cys	Thr	Cys	His									
690										695					700									
Ser	Gly	Arg	Val	Leu	Cys	Glu	Thr	Glu	Val	Cys	Pro	Pro	Leu	Leu	Cys									
705										710					715					720				
Gln	Asn	Pro	Ser	Arg	Thr	Gln	Asp	Ser	Cys	Cys	Pro	Gln	Cys	Thr	Asp									
725										730					735									
Gln	Pro	Phe	Arg	Pro	Ser	Leu	Ser	Arg	Asn	Asn	Ser	Val	Pro	Asn	Tyr									
740										745					750									
Cys	Lys	Asn	Asp	Glu	Gly	Asp	Ile	Phe	Leu	Ala	Ala	Glu	Ser	Trp	Lys									
755										760					765									
Pro	Asp	Val	Cys	Thr	Ser	Cys	Ile	Cys	Ile	Asp	Ser	Val	Ile	Ser	Cys									
770										775					780									
Phe	Ser	Glu	Ser	Cys	Pro	Ser	Val	Ser	Cys	Glu	Arg	Pro	Val	Leu	Arg									
785										790					795					800				
Lys	Gly	Gln	Cys	Cys	Pro	Tyr	Cys	Ile	Glu	Asp	Thr	Ile	Pro	Lys	Lys									
805										810					815									
Val	Val	Cys	His	Phe	Ser	Gly	Lys	Ala	Tyr	Ala	Asp	Glu	Glu	Arg	Trp									
820										825					830									
Asp	Leu	Asp	Ser	Cys	Thr	His	Cys	Tyr	Cys	Leu	Gln	Gly	Gln	Thr	Leu									
835										840					845									
Cys	Ser	Thr	Val	Ser	Cys	Pro	Pro	Leu	Pro	Cys	Val	Glu	Pro	Ile	Asn									
850										855					860									
Val	Glu	Gly	Ser	Cys	Cys	Pro	Met	Cys	Pro	Glu	Met	Tyr	Val	Pro	Glu									
865										870					875					880				
Pro	Thr	Asn	Ile	Pro	Ile	Glu	Lys	Thr	Asn	His	Arg	Gly	Glu	Val	Asp									

<b>&lt;400&gt; 75</b>						
gtgcacgcgt	ggcagacgga	gaaggccagt	gccagcttg	aaggttctgt	caccttttgc	60
agtgggtcaa	atgagaaaaa	agtggaaaat	gggaggcatg	aaatacatct	tttcgttgtt	120
gttcttttct	ttgctagaag	gaggcaaaac	agagcaagta	aaacattcag	agacatattg	180
catgtttcaa	gacaagaagt	acagagtggt	tgagagatgg	catccttacc	tggaaacctta	240
tgggttggtt	tactgcgtga	actgcatctg	ctcagagaa	gggaatgtgc	tttgcacccg	300
agtcagatgt	ccaaatgttc	attgcctttc	tctgtgcat	attcctcatc	tgtgtgccc	360
tcgtgcccc	gactccttac	ccccagtgaa	caataagggtg	accagcaagt	cttgcgagta	420
caatgggaca	acttaccaac	atggagagct	gttcgtagct	gaagggctct	ttcagaatcg	480
gcaaccacaat	caatgcaccc	agtgcagctg	ttcggaggga	aacgtgtatt	gtggtctcaa	540
gacttgcgcc	aaattaacct	gtgccttccc	agtcctctgt	ccgattcctt	gctgcccgggt	600
atgcagagga	gatggagaac	tgtcatggga	acattctgat	ggtgatattc	tcggcgcaac	660
tgccaacaga	gaagcaagac	attcttacc	ccgctctcac	tatgatcctc	caccaagccg	720
acaggctgga	ggtctgtccc	gctttcctgg	ggccagaagt	caccggggag	ctcttatgga	780
ttcccagcaa	gcattcaggaa	ccatttgtca	aattgtcatc	aataacaaac	acaagcatgg	840
acaagtgtgt	gtttccaatg	gaaagaccta	ttctcatggc	gagtcctggc	acccaaacct	900
ccgggcattt	ggcatttgtg	agtgtgtgct	atgtacttgt	aatgtacca	agcaagagtg	960
taagaaaatc	cactgcccc	atcgataccc	ctgcaagtat	cctcaaaaa	tagacggaaa	1020
gtgtgtcaag	gtgtgtccag	gtaaaaaagc	aaaagaagaa	cttccaggcc	aaagctttga	1080
caataaaaggc	tacttctcgc	gggaagaaac	gatgcctgtg	tatgagtctg	tattcatgga	1140
ggatggggag	acaaccagaa	aaatagcact	ggagactgtg	agaccacctc	aggtagaggt	1200
ccacgttttg	actattcgaa	agggcattct	ccagcacttc	catattgaga	agatctccaa	1260
gaggatgttt	gaggagcttc	ctcacttcaa	gctggtgacc	agaacaaccc	tgagcccatg	1320
gaagatcttc	accgaaggag	aagctcagat	cagccagatg	tgttcaagtc	gtgtatgcag	1380
aacagagctt	gaagatttag	tcaaggtttt	gtacctggag	agatctgaaa	agggccactg	1440

```

ttaggcaaga cagacagtat tggatagggg aaagcaagaa aactcaagct gcagctggac 1500
tgagggttta ttttgcttaa gtcaacagtg ccctaaaact ccaaactcaa atgcagctcaa 1560
ttatttcacgc catgcacagc ataatttgct cctttgtgtg gagtgggtgtg tcagcccttg 1620
aacatctcct ccaaagagac tagaagagtc ttaaattata tgtgggagga ggaggagtag 1680
aacatcacaa cactgctcta gtttcttgga gaatcacatt tctttacagg ttaaagacaa 1740
acaagacccc aggggttttta tctagaaagt tattcaagtg aaagaaagag aagggaattg 1800
cttagtagga gttctgcagt atagaacaat tacttgtagt aaattatacc tttgaatttt 1860
agaatgtcat gtgttctttt aaaaaaatta gctccccatc ctccctcctc actccctccc 1920
tccctccttc tctctctctc tctctctccc tctctcacag acacacacac acacacacac 1980
acacacacgc acgtccacac tcacattaaa cttaaagcttt atttgaagca aagctagcca 2040
aaattctacg ttacttttcc cttgactgga tcccaagtag cttggaagtt tttgtgcccc 2100
ggagagtaaa taactgtgaa caagaggctc tgcccttagg tctttgtggc tgtttaagtc 2160
accaacaata gagtccaggt aaagaataaa aacactttca tagcctcatt cattcactta 2220
gaagtggtaa taatttttcc ctaatgatac cacttttctt tccccctgt acctatggga 2280
cttcagaaaa gaagttaa atagtaaaat catcagaaac tgaatccatg taagaaaaaa 2340
taattgttga agaaagaagt tgatagaatt caaaaaggcc atctttttgc tttcacatca 2400
ataaaattta ccaagtaata gatcagtagt cactaatatt tttgagacca tagttgtctg 2460
gtcagaaaaa ttatattaaa ttagtaaat ctagaagctc tttaaaaggg aagttttcct 2520
tcttctccaa ttataggagt tgatttttac tttgcaaagt ggctcgggtc tcatgagcat 2580
ctgcatgttg actcttcagt taagaaaatt gttgttcatt tagggaggtg gatattctga 2640
tgaagatctt tatcctaaac cttctacta tcttctctt attcatcaag cagatatttt 2700
agtcaagaat tccagagaag gctgctccta aaatgtctac ttgcagccca ataccagagc 2760
ataaactatc cattctgggg tctggcttta gaaatcatct ttgtgggaag acctaattct 2820
tcacagcaag gatctcaggc atgccttcta gatttgttcc ctctgagggg caggaatgaa 2880
ctgtagaaat gttttaagga cccagaaacc ccatatgtct cattccatga ctataggtga 2940
gagaattctt tcctaagagg gtttgatacc aataggggaa aatgtaaaat gttcagctct 3000
tatgacaacc tggcataaag gagtcaattc ttatgaaaga gacacaaggg ccttatggcc 3060
agggtttctt gggacaagac tctcaccagc acatcacaca cgttctcctt ggaagagaga 3120
agcagtacat cccggttgag aggtcacaaa gcattagtgt gtgtgtgtgt gtgtgtgtgt 3180
gtgtgtgtgt gtgtgtgtgt gtgtgtatgt ggtaaagggg ggaaggtgtt 3240
atgctgctgc tccctccgtc ccagagggtg cagtgtattc ataagtgtga gactagtaac 3300
tagatcctaa ggcaaagagg tgtttctcct tttgatgat tcatcccaaa gccttccac 3360
ccagggtgtc tctgaaagct tagccttaag agaacacgca gagagtttcc ctagatatac 3420
tctgctctcc aggtgctggg acacaccttt gcaaaatgct gtgggaagca ggagctgggg 3480
agctgtgtta agtcaaagta gaaaccctcc agtggttggt gttgtgtaga gaataggaca 3540
tagggtaaaag aggccaagct gcctgtagt agtagagaag aatggatgtg gttcttcttg 3600
tgtatttatt tgatcataa acacttgga caacaagac cataagcatc atttagcagt 3660
tgtagccatt ttctagttaa ctcatgtaaa caagtaagag taacataaca gtattacct 3720
ttcactgttc tcacaggaca tgtacctaat tatggtagt atttatgtag tcaactgtatt 3780
tctggatttt taaattaata aaaaagttaa ttttgaaaa tcaaaaaaa aaaaaaaa 3840
aaaaaaaaa aaaaaaaaaa a 3861

```

&lt;210&gt; 76

&lt;211&gt; 457

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 76

```

Met Arg Lys Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu
  1             5             10             15

Leu Phe Phe Leu Leu Leu Glu Gly Gly Lys Thr Glu Gln Val Lys His
      20             25             30

Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu
      35             40             45

Arg Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn
      50             55             60

```

Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys  
 65 70 75 80  
 Pro Asn Val His Cys Leu Ser Pro Val His Ile Pro His Leu Cys Cys  
 85 90 95  
 Pro Arg Cys Pro Asp Ser Leu Pro Pro Val Asn Asn Lys Val Thr Ser  
 100 105 110  
 Lys Ser Cys Glu Tyr Asn Gly Thr Thr Tyr Gln His Gly Glu Leu Phe  
 115 120 125  
 Val Ala Glu Gly Leu Phe Gln Asn Arg Gln Pro Asn Gln Cys Thr Gln  
 130 135 140  
 Cys Ser Cys Ser Glu Gly Asn Val Tyr Cys Gly Leu Lys Thr Cys Pro  
 145 150 155 160  
 Lys Leu Thr Cys Ala Phe Pro Val Ser Val Pro Asp Ser Cys Cys Arg  
 165 170 175  
 Val Cys Arg Gly Asp Gly Glu Leu Ser Trp Glu His Ser Asp Gly Asp  
 180 185 190  
 Ile Phe Arg Gln Pro Ala Asn Arg Glu Ala Arg His Ser Tyr His Arg  
 195 200 205  
 Ser His Tyr Asp Pro Pro Pro Ser Arg Gln Ala Gly Gly Leu Ser Arg  
 210 215 220  
 Phe Pro Gly Ala Arg Ser His Arg Gly Ala Leu Met Asp Ser Gln Gln  
 225 230 235 240  
 Ala Ser Gly Thr Ile Val Gln Ile Val Ile Asn Asn Lys His Lys His  
 245 250 255  
 Gly Gln Val Cys Val Ser Asn Gly Lys Thr Tyr Ser His Gly Glu Ser  
 260 265 270  
 Trp His Pro Asn Leu Arg Ala Phe Gly Ile Val Glu Cys Val Leu Cys  
 275 280 285  
 Thr Cys Asn Val Thr Lys Gln Glu Cys Lys Lys Ile His Cys Pro Asn  
 290 295 300  
 Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Ile Asp Gly Lys Cys Cys Lys  
 305 310 315 320  
 Val Cys Pro Gly Lys Lys Ala Lys Glu Glu Leu Pro Gly Gln Ser Phe  
 325 330 335  
 Asp Asn Lys Gly Tyr Phe Cys Gly Glu Glu Thr Met Pro Val Tyr Glu  
 340 345 350  
 Ser Val Phe Met Glu Asp Gly Glu Thr Thr Arg Lys Ile Ala Leu Glu  
 355 360 365  
 Thr Glu Arg Pro Pro Gln Val Glu Val His Val Trp Thr Ile Arg Lys  
 370 375 380

Gly Ile Leu Gln His Phe His Ile Glu Lys Ile Ser Lys Arg Met Phe  
 385 390 395 400

Glu Glu Leu Pro His Phe Lys Leu Val Thr Arg Thr Thr Leu Ser Gln  
 405 410 415

Trp Lys Ile Phe Thr Glu Gly Glu Ala Gln Ile Ser Gln Met Cys Ser  
 420 425 430

Ser Arg Val Cys Arg Thr Glu Leu Glu Asp Leu Val Lys Val Leu Tyr  
 435 440 445

Leu Glu Arg Ser Glu Lys Gly His Cys  
 450 455

&lt;210&gt; 77

&lt;211&gt; 2050

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 77

```

gtgctctgag aagccggact acgcggcagc ggctcttcaa agcggagccg ggagtttttg 60
ctacagtttt cgccaccatg agtcgcagct ataatgatga gctgcagttc ttggagaaga 120
tcaataaaaa ctgctggagg atcaagaagg gcttcgtgcc caacatgcag gttgaagggtg 180
ttttctatgt gaatgatgct ctggagaaat tgatgtttga ggaattaagg aatgcctgtc 240
gaggtggttg tggtggtggc ttcctgccag ccatgaaaca gattggcaat gtggcagccc 300
tgcttggaat tggtcatcga tctattgggc ttcctgatgt ccattcagga tatgggtttg 360
ctattgggaa catggcagcc tttgatatga atgaccctga agcagtagta tccccagggtg 420
gtgtcggggt tgacatcaac tgtggtgtcc gcttgctaag aaccaattta gatgaaagtg 480
atgtccagcc tgtgaaggag caacttgccc aagctatgtt tgaccacatt cctgttgggg 540
tggttgcaaa aggtgtcatc ccaatgaatg ccaaagactt ggaggaggcc ttggagatgg 600
gggtggactg gtccttaaga gaagggtatg cctgggctga agacaaggag cactgcgagg 660
agtacggaag gatgctgcag gctgacccca ataaagtttc tgcaagggcg aagaaaagag 720
gccttcctca gttggggacc ctgggagcag gcaaccatta tgcagaaatc caggttgttg 780
atgagatttt caatgagtat gctgctaaaa aaatgggcat cgaccataag ggacaggtgt 840
gtgtgatgat ccacagtgga agcagaggct tgggccacca agtagccaca gatgcgctgg 900
tagctatgga gaaggccatg aagagagaca agattatagt caatgatcgg cagttggcct 960
gtgctcgaat cgcttcccca gaggttcaag actatctgaa gggaatggca gctgctggga 1020
actatgcctg ggtcaaccgc tcttccatga ccttcttaac cgtcaggct ttcgccaagg 1080
tcttcaacac aaccctgat gacttggacc tacatgtgat ctatgatgtt tctcacaaca 1140
ttgccaagt ggagcagcat gtggtggacg gaaaggaaag gacactgtta gtacacagga 1200
agggatccac ccgcgctttc cctcctcacc atccctcat tgctgttgat taccaactca 1260
ctggacagcc agtgctcatt ggtggcacca tgggaacctg tagttatgtt cttactggca 1320
ctgaacaggg catgactgag acctttggaa caacctgtca tggagcgggc cgtgcattgt 1380
cccgagcaaa atctcgacgt aatttagatt tccaggatgt cttagacaaa ttggcagata 1440
tggaattgc gatccgtgtt gcctcaccca aactggttat ggaagaggct cctgagtcct 1500
ataagaatgt gacagatgtg gtaaatacct gccatgatgc tggaaatcagc aagaaagcca 1560
ttaaactgag accaattgct gtgatcaaag gatagaacct tggacagcag ggctgcctga 1620
caccaccaac cctctctgaa gtggaagtgg actgacatgc tcttctgaca tcagactcaa 1680
ggcgggacaa gttgcaaagt gtgcagctgt aactgctcac gccaaaatgg ctgatgggga 1740
ggctgctgct ttcaggggcc cgtgcttgta aaataacctt ccaggaagag gcacattgcc 1800
cacctttgga aagggaggaa tatgccttct ccttggttgt tccacagagt tttaggaaaa 1860
tctgttaggg atgggtagat gtcaaactgc cttacgcagt catactgatc tttagccatc 1920
agattgatct tcttcacacc aagctctgtt tacattccga gaggtgtcat gaagaaagtt 1980
ctgttcaata agggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2040
aaaaaaaaaa

```

2050

&lt;210&gt; 78

&lt;211&gt; 505

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 78

```

Met Ser Arg Ser Tyr Asn Asp Glu Leu Gln Phe Leu Glu Lys Ile Asn
 1             5             10             15

Lys Asn Cys Trp Arg Ile Lys Lys Gly Phe Val Pro Asn Met Gln Val
      20             25             30

Glu Gly Val Phe Tyr Val Asn Asp Ala Leu Glu Lys Leu Met Phe Glu
      35             40             45

Glu Leu Arg Asn Ala Cys Arg Gly Gly Gly Val Gly Gly Phe Leu Pro
      50             55             60

Ala Met Lys Gln Ile Gly Asn Val Ala Ala Leu Pro Gly Ile Val His
      65             70             75             80

Arg Ser Ile Gly Leu Pro Asp Val His Ser Gly Tyr Gly Phe Ala Ile
      85             90             95

Gly Asn Met Ala Ala Phe Asp Met Asn Asp Pro Glu Ala Val Val Ser
      100            105            110

Pro Gly Gly Val Gly Phe Asp Ile Asn Cys Gly Val Arg Leu Leu Arg
      115            120            125

Thr Asn Leu Asp Glu Ser Asp Val Gln Pro Val Lys Glu Gln Leu Ala
      130            135            140

Gln Ala Met Phe Asp His Ile Pro Val Gly Val Gly Ser Lys Gly Val
      145            150            155            160

Ile Pro Met Asn Ala Lys Asp Leu Glu Glu Ala Leu Glu Met Gly Val
      165            170            175

Asp Trp Ser Leu Arg Glu Gly Tyr Ala Trp Ala Glu Asp Lys Glu His
      180            185            190

Cys Glu Glu Tyr Gly Arg Met Leu Gln Ala Asp Pro Asn Lys Val Ser
      195            200            205

Ala Arg Ala Lys Lys Arg Gly Leu Pro Gln Leu Gly Thr Leu Gly Ala
      210            215            220

Gly Asn His Tyr Ala Glu Ile Gln Val Val Asp Glu Ile Phe Asn Glu
      225            230            235            240

Tyr Ala Ala Lys Lys Met Gly Ile Asp His Lys Gly Gln Val Cys Val
      245            250            255

Met Ile His Ser Gly Ser Arg Gly Leu Gly His Gln Val Ala Thr Asp
      260            265            270

Ala Leu Val Ala Met Glu Lys Ala Met Lys Arg Asp Lys Ile Ile Val
      275            280            285

Asn Asp Arg Gln Leu Ala Cys Ala Arg Ile Ala Ser Pro Glu Gly Gln
      290            295            300

```

Asp Tyr Leu Lys Gly Met Ala Ala Ala Gly Asn Tyr Ala Trp Val Asn  
 305 310 315 320  
 Arg Ser Ser Met Thr Phe Leu Thr Arg Gln Ala Phe Ala Lys Val Phe  
 325 330 335  
 Asn Thr Thr Pro Asp Asp Leu Asp Leu His Val Ile Tyr Asp Val Ser  
 340 345 350  
 His Asn Ile Ala Lys Val Glu Gln His Val Val Asp Gly Lys Glu Arg  
 355 360 365  
 Thr Leu Leu Val His Arg Lys Gly Ser Thr Arg Ala Phe Pro Pro His  
 370 375 380  
 His Pro Leu Ile Ala Val Asp Tyr Gln Leu Thr Gly Gln Pro Val Leu  
 385 390 395 400  
 Ile Gly Gly Thr Met Gly Thr Cys Ser Tyr Val Leu Thr Gly Thr Glu  
 405 410 415  
 Gln Gly Met Thr Glu Thr Phe Gly Thr Thr Cys His Gly Ala Gly Arg  
 420 425 430  
 Ala Leu Ser Arg Ala Lys Ser Arg Arg Asn Leu Asp Phe Gln Asp Val  
 435 440 445  
 Leu Asp Lys Leu Ala Asp Met Gly Ile Ala Ile Arg Val Ala Ser Pro  
 450 455 460  
 Lys Leu Val Met Glu Glu Ala Pro Glu Ser Tyr Lys Asn Val Thr Asp  
 465 470 475 480  
 Val Val Asn Thr Cys His Asp Ala Gly Ile Ser Lys Lys Ala Ile Lys  
 485 490 495  
 Leu Arg Pro Ile Ala Val Ile Lys Gly  
 500 505

&lt;210&gt; 79

&lt;211&gt; 1178

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 79

gccaaatgtc cgggtcaagat gtcacacagc tccagtggct cagccagtct gagtcagggtt 60  
 tctccagggg aagaaacaga tcaaactgaa accgtgtcag ttcagtcttc ggtattgggg 120  
 aaggggtgtaa aacatcgacc cccaccaatc aaacttcctt caagctcagg aaatagttcc 180  
 tcaggtaact attttacacc acaacagaca agcagctttc tcaaattctc aactcctcct 240  
 ccttcttcta agccatcaag tattcctcgg aaatcatctg tggatctcaa tcaagtttagc 300  
 atgctttctc cagctgccct atcacctgcc agctcatcac aaagaaccac ggccaccagc 360  
 gtcattggca actctgctgg acttaacttc atcaatgtag tgggctctgt ttgtggggcc 420  
 caggctttga tgagtgttc aaaccccatg ctgggctgta aacttggtgc cataactcct 480  
 gcaggaataa acctgagcgg ccttctaccc tcaggagggtc tgctaccaa tgcactgccc 540  
 agtgcaatgc aggcagcttc tcaagcaggt gttccatttg gtttaaaaaa tacttcaagt 600  
 ctcaggccct taaatctact ccagcttcca ggtggttcac ttatttttaa cactctgcag 660  
 cagcagcaac agcagctctc ccagtttaca ccacaacaac ctcagcagcc cacaacttgt 720  
 agtctcaaac agccagggga gcagggttct gagcaagggt caaccagtca agaacaggcc 780



ttatctgctc agcaagctgc tgttattaac cttactggag taggaagttt tatgcagtca 840  
 caggcagctg cagttgcat tcttgacgca tcaaattggct atggcagcag cagcagcaca 900  
 aacagctcag ctacatcatc atcggcatac aggcagccag tcaaaaagta aaatgaagag 960  
 aggcattgcca accactccaa aattttgagt cttgcattac tttttgttcc ttttttaaaa 1020  
 acacaagagc actgaatcaa aagaattgag tttctacttt ttgttttttt taatgtgtca 1080  
 gtattttaca ttgctagatg tacaaacttt atacagaagc acaaccttat catttttaaa 1140  
 taaaaacagg gaaatggttt aacaaaaaaa aaaaaaaa 1178

<210> 80

<211> 310

<212> PRT

<213> Homo sapiens

<400> 80

Met Ser His Ser Ser Ser Gly Ser Ala Ser Leu Ser Gln Val Ser Pro  
 1 5 10 15  
 Gly Lys Glu Thr Asp Gln Thr Glu Thr Val Ser Val Gln Ser Ser Val  
 20 25 30  
 Leu Gly Lys Gly Val Lys His Arg Pro Pro Pro Ile Lys Leu Pro Ser  
 35 40 45  
 Ser Ser Gly Asn Ser Ser Ser Gly Asn Tyr Phe Thr Pro Gln Gln Thr  
 50 55 60  
 Ser Ser Phe Leu Lys Ser Pro Thr Pro Pro Pro Ser Ser Lys Pro Ser  
 65 70 75 80  
 Ser Ile Pro Arg Lys Ser Ser Val Asp Leu Asn Gln Val Ser Met Leu  
 85 90 95  
 Ser Pro Ala Ala Leu Ser Pro Ala Ser Ser Ser Gln Arg Thr Thr Ala  
 100 105 110  
 Thr Gln Val Met Ala Asn Ser Ala Gly Leu Asn Phe Ile Asn Val Val  
 115 120 125  
 Gly Ser Val Cys Gly Ala Gln Ala Leu Met Ser Gly Ser Asn Pro Met  
 130 135 140  
 Leu Gly Cys Asn Thr Gly Ala Ile Thr Pro Ala Gly Ile Asn Leu Ser  
 145 150 155 160  
 Gly Leu Leu Pro Ser Gly Gly Leu Leu Pro Asn Ala Leu Pro Ser Ala  
 165 170 175  
 Met Gln Ala Ala Ser Gln Ala Gly Val Pro Phe Gly Leu Lys Asn Thr  
 180 185 190  
 Ser Ser Leu Arg Pro Leu Asn Leu Leu Gln Leu Pro Gly Gly Ser Leu  
 195 200 205  
 Ile Phe Asn Thr Leu Gln Gln Gln Gln Gln Gln Leu Ser Gln Phe Thr  
 210 215 220  
 Pro Gln Gln Pro Gln Gln Pro Thr Thr Cys Ser Pro Gln Gln Pro Gly  
 225 230 235 240  
 Glu Gln Gly Ser Glu Gln Gly Ser Thr Ser Gln Glu Gln Ala Leu Ser

245										250					255				
Ala	Gln	Gln	Ala	Ala	Val	Ile	Asn	Leu	Thr	Gly	Val	Gly	Ser	Phe	Met				
260										265					270				
Gln	Ser	Gln	Ala	Ala	Ala	Val	Ala	Ile	Leu	Ala	Ala	Ser	Asn	Gly	Tyr				
275										280					285				
Gly	Ser	Ser	Ser	Ser	Thr	Asn	Ser	Ser	Ala	Thr	Ser	Ser	Ser	Ala	Tyr				
290										295					300				
Arg	Gln	Pro	Val	Lys	Lys														
305										310									

```
<210> 81
<211> 641
<212> DNA
<213> Homo sapiens
```

<400> 81							
gacgatgtca	ccctgtcctc	cctccttgtc	tcttgtctctg	ctaactcaac	tctgccttcc	60	
tctttttcat	tcttctactc	tgccctatat	ggaggacaaa	tggacaccag	gggtgctaac	120	
cttatttggtg	cctgccccag	cctaccccag	gtgccagcag	actctcgtgc	acaggaggct	180	
ccccaggtta	tggagccagg	aagaaatttc	tctgcactgg	atggactgta	tattgagatt	240	
aaaaaattata	tctcttatat	tctcgtctat	atcaatgtc	tctctgtaaa	acctcttcc	300	
agcctcattt	ctctcaactg	atcttgttta	ggcgttgtat	tctttttatt	tactctttgc	360	
ttgactgctt	cctcctaacc	ctctaccac	tagcactcta	cttctctaa	ctgttgtgtc	420	
attaactctg	ttggatcaac	tctctgggaa	aagattctgt	taatgtaagt	gcacttactc	480	
cttggatgtg	gtcatagtc	tagtggtctt	tgctaaataa	acctttctta	tttctaaaaa	540	
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	600	
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	a		64	

```
<210> 82
<211> 94
<212> PRT
<213> Homo sapiens
```

```

<400> 82
Met Ser Pro Cys Pro Pro Ser Leu Leu Leu Ala Leu Leu Thr Gln Leu
  1                      5                      10                      15

Cys Leu Pro Leu Phe His Ser Ser Thr Leu Pro Tyr Met Glu Asp Lys
      20                      25                      30

Trp Thr Pro Gly Val Leu Thr Leu Leu Val Pro Ala Pro Ala Tyr Pro
      35                      40                      45

Arg Cys Gln Gln Thr Leu Val His Arg Arg Leu Pro Gln Leu Trp Ser
      50                      55                      60

Gln Glu Arg Ile Ser Leu His Trp Met Asp Cys Ile Leu Arg Leu Lys
  65                      70                      75                      80

Ile Ile Phe Leu Ile Phe Leu Leu Ile Ser Met Leu Ser Leu
      85                      90

```

<210> 83  
<211> 832

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 83

```

ccttgcatta ccttcttctg ccctatctgc tgctaggtgt aaacctgttt tttttcaccc 60
tgacttggtg aaccaatcct ggcattataa caaaagcaaa tgaattatta tttcttcacg 120
tttatgaatt tgatgaagtg atgtttccaa agaactgtgag gtgctctact tgtgatttaa 180
ggaaccagc tcgatccaag cactgcagtg tgtgtaactg gtgtgtgcac cgtttcgacc 240
atcactgtgt ttgggtgaac aactgcatcg gggcctggaa catcaggtac ttcctcatct 300
acgtcttgac cttgacggcc tcggctgcc aacgtcgccat tgtgagcacc acttttctgg 360
tcacttggt ggtgatgtca gattataacc aggagactta catcgatgac cttggacacc 420
ttccatgtta tggacacggc cttcttatt cagtacctgt tcctgacttt tccacggatt 480
gtcttcacgc tgggctttgt cgtggttctg agcttcctcc tgggtggcta cctgttggtt 540
gtcctgtatc tggcggccac caaccagact actaacgagt ggtacagagg tgactgggcc 600
tggtgccagc gttgtccct tgtggcctgg cctccgtcag cagagcccca agtccaccgg 660
aacattcact cccatgggct tcggagcaac cttcaagaga tctttctacc tgcctttcca 720
tgcatgaga ggaagaaaca agaatgaca gtgtatgact gcctttgagc tgtagttccc 780
gtttatttac acatgtggat cctcgtttcc ctcccattg aattctagac ct 832

```

&lt;210&gt; 84

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 84

```

Met Phe Pro Lys Asn Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro
  1              5              10              15

Ala Arg Ser Lys His Cys Ser Val Cys Asn Trp Cys Val His Arg Phe
      20              25              30

Asp His His Cys Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile
      35              40              45

Arg Tyr Phe Leu Ile Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr
      50              55              60

Val Ala Ile Val Ser Thr Thr Phe Leu Val His Leu Val Val Met Ser
      65              70              75              80

Asp Leu Tyr Gln Glu Thr Tyr Ile Asp Asp Leu Gly His Leu Pro Cys
      85              90              95

Tyr Gly His Gly Leu Ser Tyr Ser Val Pro Val Pro Asp Phe Ser Thr
      100              105              110

Asp Cys Leu His Ala Gly Leu Cys Arg Gly Ser Glu Leu Pro Pro Gly
      115              120              125

Trp Leu Pro Val Val Cys Pro Val Ser Gly Gly His Gln Pro Asp Tyr
      130              135              140

```

&lt;210&gt; 85

&lt;211&gt; 3790

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 85

```

aacggcagtc tcaatctggc cccacacctt tcttgggctt gtaggaaggt ggacatgggc 60

```

```

tcccggagac aagacaagtg atatgttgaa ctgttcggtg gctggaatca actgctcctg 120
gagtgcaccta aggcacagtgt ttatcagaac ttagccaggg ccagccaagc aggcacagat 180
gctctgctat gaaatgccac gcaggcagag actgacaagc ggtaggaact gagctttccc 240
cttgactgc tgcttctgc tgtgttcagg ggagggggtc actttctggc aactctgctg 300
ctgctgctgc tgctgctgct acttcagctt cctctccact caaggtaagc aggctaaggg 360
agggcaggct gctagggaaa gctttgtacc atgaacagga tccgaaagtt tttccgagga 420
agtgggagcag tcttggcatt tatctttgta gcttctgtca tctggctcct ctttgacatg 480
gcagctctcc gcctctcatt .cagtgcagtc aacactcggg tcatcaagga agacattgtg 540
aggagggagc ggataggatt cagagttcag ccagaccaag gaaaaatttt ttacagcagc 600
ataaaagaga tgaaacctcc cctaagggga catgggaaag gggcatgggg caaagagaat 660
gttagaaaaa ctgaggagag tgtgtcctcaag gttgaggtgg acttgagacca aaccagagg 720
gaaagaaaaa tgcagaatgc cctgggaagg ggcaaggttg tgccgttgtg gcctcctgca 780
catctgcaga ccctccctgt gactcctaac aagcagaaga cagacgggag aggcaccaa 840
cctgaagcct cctctcacca ggggacacca aagcaaacga cagctcaggg ggctccaaag 900
acctcattca tagcagcaaa aggaactcag gtagtcaaaa tatcagtaca catgggacgt 960
gtcagtttaa aacaggagcc ccggaagagt catagtccca gcagtgcacac atcaaaacta 1020
gcagctgaaa gggacttgaa tgtgaccatc agtcttagta ctgatagacc aaagcagcga 1080
tcacaggcag tagcaaacga gagggcacac cctgccagca cagcagtgcc gaagtctggg 1140
gaagccatgg ccttaaacaa aactaagact cagagcaaaag aagtcaatgc aaataaacac 1200
aaagccaata cgagtcttcc ttttcctaag ttcactgtca attcaaatcg ctttaaggaa 1260
caatctatta atgagacacc tttgggaagt ttgtcaagg atgatggagc tagaggggct 1320
catgggaaga aactcaattt ctctgaaagc catcttgtga ttataacca agaggaagag 1380
caaaaggcag accccaaaga ggtctctaat tctaaaacca aaacaatatt tcctaaagta 1440
ttgggtaaaa gccaaagtaa acacatttcc aggaatagaa gtgagatgtc ttcctcttca 1500
cttgctccac atagagtgc actgtcccaa actaaccatg ctttaactgg agggctagag 1560
ccagcaaaaa tcaacataac tgccaaagcc ccctctacag aatacaacca gagtcatata 1620
aaagcccttt tacctgaaga cagtggaaag caccagggtg taagaattga tgtgacactt 1680
tctccaaggg accccaaagc tccagggcag tttgggcgtc ctgtagttgt ccccatgga 1740
aaggagaagg aggcagaaag aagatggaaa gaaggaaact tcaatgtcta ccttagcgat 1800
ttgatccag tggatagagc cattgaagac accagacctg ctggatgtgc agagcagcta 1860
gttcacaata acctccaac caccagtgtc atcatgtgtc ttgtggatga agtgtggtcc 1920
actctctga gatctgttca cagtgtcctc aatcgctctc ctccacacct catcaaggag 1980
attctgctgg tagatgactt cagcaccaaa gactatctaa aagataattt ggataaaatac 2040
atgtcccagt ttccaaaagt tcggattctt cgctcaaag agagacatgg ctttaataagg 2100
gccaggctgg caggagcaca gaatgcaaca ggtgatgtgt tgacattttt agattctcat 2160
gtggaatgta acgttggttg gttggaacct cttctggaaa gagttttatt aagtagaaag 2220
aaagtggcct gtccagtaat cgaagtcatc aatgataagg atatgagtta catgacagt 2280
gataactttc aaagaggcat ctttgtgtgg ccatgaact ttggttgag aacaattcct 2340
ccagatgtca ttgcaaaaaa cagaattaaa gaaactgata caataagggt ccctgtcatg 2400
gctgggggat tgttttctat tgacaaaagt tacttttttg aacttggaa atacgacct 2460
ggccttgatg tttgggttg ggaaaatatg gagctctcat tcaagggtgt gatgtgtggt 2520
ggtgaaattg agatcattcc ctgctcccga gtgggccata tattcagaaa tgacaatcca 2580
tattccttcc ccaaagaccg gatgaagaca gtggagcgga acttgggtgc ggttgccgag 2640
gtctggtggt atgagtataa ggagctgttc tatggccatg gagaccacct catcgacca 2700
gggctagatg ttggcaacct caccagcaa agggagctgc gaaagaaact gaagtgcaa 2760
agtttcaaat ggtacttgga gaatgtctt cctgacttaa gggctcccat tgtgagagct 2820
agtgggtgtc ttattaatgt ggctttgggt aaatgcattt ccattgaaa cactacagt 2880
attctggaag actgcgatg gagcaagag ctcaacaat ttaattacac ctggttaaga 2940
cttattaaat gtggagaatg gtgtatagcc ccatccctg ataaaggagc cgtaaggctg 3000
caccctgtg ataacagaaa caaagggtc aaatggctgc ataaatcaac atcagtctt 3060
catccagaac tggatgaatc cattgtttt gaaaacaatc agcaattatt atgcttgga 3120
ggaaattttt ctcaaaagat cctgaaagta gctgctgtg acccagtga gccatatcaa 3180
aagtggaaat ttgaaaaata ttatgaagcc tgaagtgtaa ctgatgtttt tatatagtaa 3240
accattaaa tactgtgaaa ataacactga acttggaac tatatttctc agcgtagtt 3300
taaattttca attttaataa catttgaatg gaagattttt tataaatcac aatatttgga 3360
ataccaaaag atgactcagg aaaacagtcc aacattggac tgaagtcctt cttcggaa 3420
gggtggcctt tgaattgcct gctttccacc ctatgctaga cctcatcatg caaatttccc 3480
tgtgaaagct aacaggtaac tggaaatgaa gcagaagga cttgagaaag catgaggata 3540
ttcccaatga ctatgtttg taataatcag ctcttctggc ccacaagtag gaatgatcaa 3600
tgagaactta acttagtcct ttatttgggg attttttcat caaacaataa tttcttgagt 3660

```

tcttatggct agaagacctc agatgccac agctgtcacg tttgtgaaat ccctccagac 3720  
 tacatgcatg cttacctaac agtttgaaat agtattgatc tactgctggt aaaaaaaaaa 3780  
 aaaaaaaaaa 3790

<210> 86

<211> 940

<212> PRT

<213> Homo sapiens

<400> 86

Met Asn Arg Ile Arg Lys Phe Phe Arg Gly Ser Gly Arg Val Leu Ala  
 1 5 10 15

Phe Ile Phe Val Ala Ser Val Ile Trp Leu Leu Phe Asp Met Ala Ala  
 20 25 30

Leu Arg Leu Ser Phe Ser Glu Ile Asn Thr Arg Val Ile Lys Glu Asp  
 35 40 45

Ile Val Arg Arg Glu Arg Ile Gly Phe Arg Val Gln Pro Asp Gln Gly  
 50 55 60

Lys Ile Phe Tyr Ser Ser Ile Lys Glu Met Lys Pro Pro Leu Arg Gly  
 65 70 75 80

His Gly Lys Gly Ala Trp Gly Lys Glu Asn Val Arg Lys Thr Glu Glu  
 85 90 95

Ser Val Leu Lys Val Glu Val Asp Leu Asp Gln Thr Gln Arg Glu Arg  
 100 105 110

Lys Met Gln Asn Ala Leu Gly Arg Gly Lys Val Val Pro Leu Trp His  
 115 120 125

Pro Ala His Leu Gln Thr Leu Pro Val Thr Pro Asn Lys Gln Lys Thr  
 130 135 140

Asp Gly Arg Gly Thr Lys Pro Glu Ala Ser Ser His Gln Gly Thr Pro  
 145 150 155 160

Lys Gln Thr Thr Ala Gln Gly Ala Pro Lys Thr Ser Phe Ile Ala Ala  
 165 170 175

Lys Gly Thr Gln Val Val Lys Ile Ser Val His Met Gly Arg Val Ser  
 180 185 190

Leu Lys Gln Glu Pro Arg Lys Ser His Ser Pro Ser Ser Asp Thr Ser  
 195 200 205

Lys Leu Ala Ala Glu Arg Asp Leu Asn Val Thr Ile Ser Leu Ser Thr  
 210 215 220

Asp Arg Pro Lys Gln Arg Ser Gln Ala Val Ala Asn Glu Arg Ala His  
 225 230 235 240

Pro Ala Ser Thr Ala Val Pro Lys Ser Gly Glu Ala Met Ala Leu Asn  
 245 250 255

Lys Thr Lys Thr Gln Ser Lys Glu Val Asn Ala Asn Lys His Lys Ala  
 260 265 270

Asn Thr Ser Leu Pro Phe Pro Lys Phe Thr Val Asn Ser Asn Arg Leu  
 275 280 285  
 Arg Lys Gln Ser Ile Asn Glu Thr Pro Leu Gly Ser Leu Ser Lys Asp  
 290 295 300  
 Asp Gly Ala Arg Gly Ala His Gly Lys Lys Leu Asn Phe Ser Glu Ser  
 305 310 315 320  
 His Leu Val Ile Ile Thr Lys Glu Glu Glu Gln Lys Ala Asp Pro Lys  
 325 330 335  
 Glu Val Ser Asn Ser Lys Thr Lys Thr Ile Phe Pro Lys Val Leu Gly  
 340 345 350  
 Lys Ser Gln Ser Lys His Ile Ser Arg Asn Arg Ser Glu Met Ser Ser  
 355 360 365  
 Ser Ser Leu Ala Pro His Arg Val Pro Leu Ser Gln Thr Asn His Ala  
 370 375 380  
 Leu Thr Gly Gly Leu Glu Pro Ala Lys Ile Asn Ile Thr Ala Lys Ala  
 385 390 395 400  
 Pro Ser Thr Glu Tyr Asn Gln Ser His Ile Lys Ala Leu Leu Pro Glu  
 405 410 415  
 Asp Ser Gly Thr His Gln Val Leu Arg Ile Asp Val Thr Leu Ser Pro  
 420 425 430  
 Arg Asp Pro Lys Ala Pro Gly Gln Phe Gly Arg Pro Val Val Val Pro  
 435 440 445  
 His Gly Lys Glu Lys Glu Ala Glu Arg Arg Trp Lys Glu Gly Asn Phe  
 450 455 460  
 Asn Val Tyr Leu Ser Asp Leu Ile Pro Val Asp Arg Ala Ile Glu Asp  
 465 470 475 480  
 Thr Arg Pro Ala Gly Cys Ala Glu Gln Leu Val His Asn Asn Leu Pro  
 485 490 495  
 Thr Thr Ser Val Ile Met Cys Phe Val Asp Glu Val Trp Ser Thr Leu  
 500 505 510  
 Leu Arg Ser Val His Ser Val Ile Asn Arg Ser Pro Pro His Leu Ile  
 515 520 525  
 Lys Glu Ile Leu Leu Val Asp Asp Phe Ser Thr Lys Asp Tyr Leu Lys  
 530 535 540  
 Asp Asn Leu Asp Lys Tyr Met Ser Gln Phe Pro Lys Val Arg Ile Leu  
 545 550 555 560  
 Arg Leu Lys Glu Arg His Gly Leu Ile Arg Ala Arg Leu Ala Gly Ala  
 565 570 575  
 Gln Asn Ala Thr Gly Asp Val Leu Thr Phe Leu Asp Ser His Val Glu  
 580 585 590

Cys Asn Val Gly Trp Leu Glu Pro Leu Leu Glu Arg Val Tyr Leu Ser  
 595 600 605  
 Arg Lys Lys Val Ala Cys Pro Val Ile Glu Val Ile Asn Asp Lys Asp  
 610 615 620  
 Met Ser Tyr Met Thr Val Asp Asn Phe Gln Arg Gly Ile Phe Val Trp  
 625 630 635 640  
 Pro Met Asn Phe Gly Trp Arg Thr Ile Pro Pro Asp Val Ile Ala Lys  
 645 650 655  
 Asn Arg Ile Lys Glu Thr Asp Thr Ile Arg Cys Pro Val Met Ala Gly  
 660 665 670  
 Gly Leu Phe Ser Ile Asp Lys Ser Tyr Phe Phe Glu Leu Gly Thr Tyr  
 675 680 685  
 Asp Pro Gly Leu Asp Val Trp Gly Gly Glu Asn Met Glu Leu Ser Phe  
 690 695 700  
 Lys Val Trp Met Cys Gly Gly Glu Ile Glu Ile Ile Pro Cys Ser Arg  
 705 710 715 720  
 Val Gly His Ile Phe Arg Asn Asp Asn Pro Tyr Ser Phe Pro Lys Asp  
 725 730 735  
 Arg Met Lys Thr Val Glu Arg Asn Leu Val Arg Val Ala Glu Val Trp  
 740 745 750  
 Leu Asp Glu Tyr Lys Glu Leu Phe Tyr Gly His Gly Asp His Leu Ile  
 755 760 765  
 Asp Gln Gly Leu Asp Val Gly Asn Leu Thr Gln Gln Arg Glu Leu Arg  
 770 775 780  
 Lys Lys Leu Lys Cys Lys Ser Phe Lys Trp Tyr Leu Glu Asn Val Phe  
 785 790 795 800  
 Pro Asp Leu Arg Ala Pro Ile Val Arg Ala Ser Gly Val Leu Ile Asn  
 805 810 815  
 Val Ala Leu Gly Lys Cys Ile Ser Ile Glu Asn Thr Thr Val Ile Leu  
 820 825 830  
 Glu Asp Cys Asp Gly Ser Lys Glu Leu Gln Gln Phe Asn Tyr Thr Trp  
 835 840 845  
 Leu Arg Leu Ile Lys Cys Gly Glu Trp Cys Ile Ala Pro Ile Pro Asp  
 850 855 860  
 Lys Gly Ala Val Arg Leu His Pro Cys Asp Asn Arg Asn Lys Gly Leu  
 865 870 875 880  
 Lys Trp Leu His Lys Ser Thr Ser Val Phe His Pro Glu Leu Val Asn  
 885 890 895  
 His Ile Val Phe Glu Asn Asn Gln Gln Leu Leu Cys Leu Glu Gly Asn  
 900 905 910

Phe Ser Gln Lys Ile Leu Lys Val Ala Ala Cys Asp Pro Val Lys Pro  
 915 920 925

Tyr Gln Lys Trp Lys Phe Glu Lys Tyr Tyr Glu Ala  
 930 935 940

<210> 87  
 <211> 1200  
 <212> DNA  
 <213> Homo sapiens

<400> 87  
 ggcttctcgg agcggcgctg ggcgaccgga gcagggtcga gatgtcctac atccccgggcc 60  
 agccggtcac cgccgtggtg caaagagttg aaattcaciaa gctgcgtcaa ggtgagaact 120  
 taatcctggg ttccagcatt ggaggtggaa tcgaccagga tccttcccag aatcccttct 180  
 atgaagacaa gacggacaag ggtatttatg tcacacgggt gtctgaagga ggccctgctg 240  
 aaatcgctgg gctgcagatt ggagacaaga tcatgcaggt gaacggctgg gacatgacca 300  
 ttgtcacaca cgaccaggcc cgcaagcggc tcaccaagcg ctccggaggag gtggtgcgtc 360  
 tgctggtgac gcggcagtcg ctgcagaagg cgtgcagcag tcatgctgtc ctacgagcca 420  
 ccaccatctg cgactcctgc ctgccgcctc tctgtacagt aacgccactt ccacactctg 480  
 tccccatctg gcttctgctg accagcttct tctcctggac accgaggatt ggaaataagg 540  
 gcctggagct gactagtagc cagtctgctg tgaccacagg ctccaggtccg accctgctgc 600  
 ttggccacag cagtggctgg gcaagtggga accactatct cttgggagcc cccaaaagct 660  
 gggaaatgct ggaggaacca ggcctttccc gcttttgctt ggctgcaggg ttgggctccg 720  
 cccctgcccc ccagccttgg tgtgtccaca ccgcagtgct tctgcccctc gggggactgg 780  
 acacacatcc tgccagaggc gctacgaagc ttgtcccaga tgaagccagg tgggctccgc 840  
 gttcactccc actctcccga ggggtgctgg cctccccagg gtttgccttc ttacggattt 900  
 agacgaggtt cgaggctcac ctatcagggc agctctcagg attgtcattt tcctctttgc 960  
 ctgtgggttt aactttttga tttttttaat cacaagtttg atacaaaatg tttttatcgt 1020  
 actctttgga gatgccatt ctacttttga atttagcttt tactaattcg catctggaag 1080  
 ctcagcaagt gcacaagcct tacttttggtt accgtggaaa ccactgccgc cctccccga 1140  
 tgtggtgtgc tgaataaaaa tgctggaatt caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200

<210> 88  
 <211> 286  
 <212> PRT  
 <213> Homo sapiens

<400> 88  
 Met Ser Tyr Ile Pro Gly Gln Pro Val Thr Ala Val Val Gln Arg Val  
 1 5 10 15  
 Glu Ile His Lys Leu Arg Gln Gly Glu Asn Leu Ile Leu Gly Phe Ser  
 20 25 30  
 Ile Gly Gly Gly Ile Asp Gln Asp Pro Ser Gln Asn Pro Phe Tyr Glu  
 35 40 45  
 Asp Lys Thr Asp Lys Gly Ile Tyr Val Thr Arg Val Ser Glu Gly Gly  
 50 55 60  
 Pro Ala Glu Ile Ala Gly Leu Gln Ile Gly Asp Lys Ile Met Gln Val  
 65 70 75 80  
 Asn Gly Trp Asp Met Thr Met Val Thr His Asp Gln Ala Arg Lys Arg  
 85 90 95  
 Leu Thr Lys Arg Ser Glu Glu Val Val Arg Leu Leu Val Thr Arg Gln



100	105	110
Ser Leu Gln Lys Ala Cys Ser Ser His Ala Val Leu Ala Ala Thr Thr		
115	120	125
Ile Cys Asp Ser Cys Leu Pro Pro Leu Cys Thr Val Thr Pro Leu Pro		
130	135	140
His Ser Val Pro Ile Trp Leu Leu Leu Thr Ser Phe Leu Ser Trp Thr		
145	150	155
		160
Pro Arg Ile Gly Asn Lys Gly Leu Glu Leu Ser Ser Ser Gln Ser Ala		
165	170	175
Val Thr Thr Gly Ser Gly Pro Thr Leu Leu Leu Gly His Ser Ser Gly		
180	185	190
Trp Ala Ser Gly Asn His Tyr Leu Leu Gly Ala Pro Lys Ser Trp Glu		
195	200	205
Met Leu Glu Glu Pro Gly Leu Ser Arg Phe Cys Leu Ala Ala Gly Leu		
210	215	220
Gly Ser Ala Pro Ala Pro Gln Pro Trp Cys Val His Thr Ala Val Leu		
225	230	235
		240
Leu Pro Leu Gly Gly Leu Asp Thr His Pro Ala Arg Gly Ala Thr Lys		
245	250	255
Leu Cys Pro Asp Glu Ala Arg Trp Ala Pro Arg Ser Leu Pro Leu Ser		
260	265	270
Arg Gly Val Leu Ala Ser Pro Gly Phe Ala Phe Leu Arg Ile		
275	280	285

<210> 89  
 <211> 1023  
 <212> DNA  
 <213> Homo sapiens

<400> 89  
 ccaacatgga gactttgtac cgtgtcccg tcttagtgct cgaatgtccc aacctgaagc 60  
 tgaagaagcc gccctgggtg cacatgccgt cggccatgac tgtgtatgct ctggtggtgg 120  
 tgtcttactt cctcatcacc ggaggaataa tttatgatgt tattgttgaa cctccaagtg 180  
 tcggttctat gactgatgaa catgggcac agaggccagt agctttcttg gcctacagag 240  
 taaatggaca atatattatg gaaggacttg catccagctt cctatttaca atgggaggtt 300  
 taggtttcat aatcctggac cgatcgaatg caccaaataat cccaaaactc aatagattcc 360  
 ttcttctggt cattggattc gtctgtgtcc tattgagttt ttcatggct agagtattca 420  
 tgagaatgaa actgccgggc tatctgatgg gttagagtgc ctttgagaag aaatcagtgg 480  
 atactggatt tgctcctgtc aatgaagttt taaaggctgt accaatcctc taatatgaaa 540  
 tgtggaagaa aatgaagagc agcagtaaaa gaaatatcta gtgaaaaaac aggaagcgta 600  
 ttgaagcttg gactagaatt tcttcttggg attaaagaga caagtttatc acagaatttt 660  
 ttttctgct ggctattgc tataccaatg atgttgagtg gcattttctt tttagttttt 720  
 cattaaaata tattccatat ctacaactat aatatcaaata aaagtgatta ttttttcaaa 780  
 cctcttaac attttttgga gatgacattt ctgattttca gaaattaaca taaaatccag 840  
 aagcaagatt ccgtaagctg agaactctgg acagttgatc agctttacct atggtgcttt 900  
 gcctttaact agagtgtgtg atggttagatt atttcagata tgtatgtaaa actgtttcct 960  
 gaacaataag atgtatgaac ggagcagaaa taaatacttt ttctaattaa aaaaaaaaaa 1020  
 aaa 1023

<210> 90  
 <211> 149  
 <212> PRT  
 <213> Homo sapiens

<400> 90  
 Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn  
           1                  5                  10                  15  
 Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr  
                   20                  25                  30  
 Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile  
           35                  40                  45  
 Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp  
           50                  55                  60  
 Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn  
           65                  70                  75                  80  
 Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met  
                   85                  90                  95  
 Gly Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile  
           100                  105                  110  
 Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val  
           115                  120                  125  
 Leu Leu Ser Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro  
           130                  135                  140  
 Gly Tyr Leu Met Gly  
 145

<210> 91  
 <211> 3901  
 <212> DNA  
 <213> Homo sapiens

<400> 91  
 gccatggagg gagtgagcgc gctgctggcc cgctgcccc aaggccggcct ggccggcggc 60  
 ctgggggtca cggcgtgcgc cgcggccggc gtgttgctct accggatcgc gcggaggatg 120  
 aagccaacgc acacgatggt caactgctgg ttctgcaacc aggatacgt ggtgccctat 180  
 gggaaccgca actgctggga ctgtccccac tgcgagcagt acaacggctt ccaggagaac 240  
 ggcgactaca acaagccgat ccccgcccag tacttgagc acctgaacca cgtggtgagc 300  
 agcgcgccca gcctgcgcga cccttcgcag ccgcagcagt gggtagcag ccaagtcctg 360  
 ctgtgcaaga ggtgcaacca ccaccagacc accaagatca agcagctggc cgccttcgct 420  
 ccccgcgagg agggcaggta tgacgaggag gtcgaggtgt accggcatca cctggagcag 480  
 atgtacaagc tgtgcgggcc gtgccaagcg gctgtggagt actacatcaa gcaccagaac 540  
 cgccagctgc gcgccctgtt gctcagccac cagttcaagc gccgggaggc cgaccagacc 600  
 caggcacaga acttctcttc cgccgtgaag tccccggtcc aggtcctcct gtcctgtgcc 660  
 ctgccttcc tggcctgcgc ctctctactg accaccgcgc tgtatggggc cagcggacac 720  
 ttgcgccag gcaccactgt gcccttgcc ctgccacctg gtggcaatgg ctcagccaca 780  
 cctgacaatg gcaccacccc tggggccgag ggtggcggc agttgctggg cctactcccc 840  
 gagcacatgg cggagaagct gtgtgaggcc tgggcctttg ggcagagcca ccagacgggc 900  
 gtcgtggcac tgggcctact cacctgcctg ctggcaatgc tgctggctgg ccgcatcagg 960

```

ctcggagga tcatgcctt ctgcacctgc ctgtgggccc tgctgctggg gctgcacctg 1020
gctgaacagc acctgcaggc cgctcgcctt agctggctaa acacgctcaa gttcagcacc 1080
acatctttgt gctgcctggt tggcttcacg gcggctgtgg ccacaaggaa ggcaacgggc 1140
ccacggaggt tccggccccg aaggtcagag aagcagccat gactgcgggg ggaggacaca 1200
cggatgtctc ggcccaggct ttgccaggtc cgaagcgggc cctctctgtt cctgcctctt 1260
ttcacctgct cagcctctcc cccccccacc ctacagcccc aggtcctggc ccagtccctc 1320
cactgcctcg aagagtcagt ctgccctgcc ttttctcttc gggcaccacc agccatcccc 1380
gagtgcctcg tagccactca ccaactgctg cactctcttg gccaatggcc ctttactagg 1440
cctgggtgact ggaatgtggg cagcgcccac acaggctctg gcccatggct tcctactggc 1500
agctccaggc accccctctt caccacgcg tttgtgtggc ctgacactgt tgggtgaggg 1560
tcctggtcct gctgtcttcc ctctgtgctt ctgcacaggg gtggtgacag tgggtacagg 1620
ctgggccccct gggtgtccct gaccgtgcag cagagtggag ctggggcagc agagagcccc 1680
agcctcacc ctgaggagca cctgtgtgtt gtcccttggt tcctgcttat ggctggaccg 1740
gcctgcagg aggtgtgtga gccgtgaagg aggccgagct gcagctctgg ctgctgcttg 1800
gcctcctgct ccaagacctt cccgagctcc cggaaatgga gagtgcagtt cttggggcca 1860
gcctggcctt cgcctatgag ttggggagcg agacccacc tgagacaggc agtaggagcc 1920
tgtgtgctgac ttgggggaatc tgagcttttc caagggtaa gggcccaggg tatgcaggcc 1980
ttcagtgcac tcaggtcgtt gtcatccttt cctcctctga cctgtcacga gcctctgcag 2040
gtgcctgctc accatggccc agcgccactc tgcctcctga ctcaggtgag ggggcagccc 2100
acagacctgc tcctcagtag cagggcctgg ccagggccct gctgttctca gcctcagttt 2160
gccatctatg aatgaggtg gacccctctc catagccctt ggggtgccag tcagtgggtg 2220
tggggatcac atgaggtggc tcatgaggac acactctgga agtcgagggg ctgccacgtg 2280
cagaggaagt tcccgccctg ggggctttat ccaggggtcc cagtcgagag tggcccagg 2340
ccgtccctca ccgggcatgt tccctctggc tgcccactcc ctccaggccc acatgtcctg 2400
ccactcgcca ctctgagcac gagttcacct tccagatgtg gccagggtgt gccagctcct 2460
ctctcctgtg cgttggaaac ccgggggagg caagagcaga tcacagggtg atgagggtta 2520
caccgctcac ctgggtctgc cgggatgggt tgggggggca ggtgccaggc ctactgctg 2580
tgaatctgcc acgcctgggg gtccctagagg ctgccccacc ccagtgattg ggtagcagct 2640
cacatcccac cagcttcac aagttaggaa ccagggtgca tcgggagacc ctccgggggt 2700
tctgtggcct ctgtgcccga tgacctgctg ggcttcagac aaggccccag cgttactggg 2760
ctcagcttgt tgttctgtgt ggagcgtgag gtgagaaac ccctctgaaa agatgtggtc 2820
ggggccacgc tccccactgg ttctgcagtg aggtgtggg gcgggtgagc caaagcggcc 2880
ccccatgggt tctacctgag gggcagggaa ccgcctgcct gtgcactcac gccaccccc 2940
agccacacaa gagcccatct gagagaagga cgtggtggag ccaggacggg aaagcgtcct 3000
gtcggtggc catgctgttg cttgctcttc gaatcttcgg ttctcgagga agtgttgaca 3060
gtgtgatgct aatgtctgct tttcttggcg ttgggtagaa gcaggacatc tgtgtgtatg 3120
tgcgtattta aattagatta ttataataa ccagagccag ccctcgcgct ggccaggatc 3180
ctcctgccga gctgatgtcg ctctgccc ctgcccgggt ccggaagcga catctcagga 3240
ggtagctctc agcagagtga ggattcctgc cttctgtaga gttttgtgtg acttttttaa 3300
ttattcatgt gtcccttaaa agtttacta cgtggagaaa attccagcac caagtgtgt 3360
ggcaacagct gagagagtgc aggcaccact gtgtgtggc ttgttgaccg ggaatgtgtc 3420
accctgccca gggaactctt ctctcgcgg gggacttggg atggccatca gacctctag 3480
ggtctggctg gggtcacct aggtatgggt gaccgtccct gagacataag cgaggtagat 3540
tcagccatcc tcacctcag acttgaggtc cccaccagg ccaagccggc ccccgctacc 3600
ccttgccctg gagcaaacg ccaggacgca gcctccacgc cgcacctgcc acattcagcc 3660
ctgcccagga aggaacacat gaccttctg tctgtgactg ttgctgagtc tctgtctcat 3720
gtcgtagaat tgttgataat tgtctagtga cctctctatc actgtaacca tcgcgcctgg 3780
cctagatgtc gtgttttggg tgctgtgttt tcaataaatg cctctggggc cctgctttta 3840
ccaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3900
a 3901

```

&lt;210&gt; 92

&lt;211&gt; 392

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 92

Met Glu Gly Val Ser Ala Leu Leu Ala Arg Cys Pro Thr Ala Gly Leu  
1 5 10 15

Ala Gly Gly Leu Gly Val Thr Ala Cys Ala Ala Ala Gly Val Leu Leu  
                   20                                  25                                  30  
 Tyr Arg Ile Ala Arg Arg Met Lys Pro Thr His Thr Met Val Asn Cys  
                   35                                  40                                  45  
 Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn Arg Asn Cys  
                   50                                  55                                  60  
 Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln Glu Asn Gly  
                   65                                  70                                  75                                  80  
 Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His Leu Asn His  
                                   85                                  90                                  95  
 Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln Pro Gln Gln  
                                   100                                  105                                  110  
 Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn His His Gln  
                   115                                  120                                  125  
 Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg Glu Glu Gly  
                   130                                  135                                  140  
 Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu Glu Gln Met  
                   145                                  150                                  155                                  160  
 Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr Tyr Ile Lys  
                                   165                                  170                                  175  
 His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His Gln Phe Lys  
                                   180                                  185                                  190  
 Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser Ser Ala Val  
                   195                                  200                                  205  
 Lys Ser Pro Val Gln Val Ile Leu Leu Arg Ala Leu Ala Phe Leu Ala  
                   210                                  215                                  220  
 Cys Ala Phe Leu Leu Thr Thr Ala Leu Tyr Gly Ala Ser Gly His Phe  
                   225                                  230                                  235                                  240  
 Ala Pro Gly Thr Thr Val Pro Leu Ala Leu Pro Pro Gly Gly Asn Gly  
                                   245                                  250                                  255  
 Ser Ala Thr Pro Asp Asn Gly Thr Thr Pro Gly Ala Glu Gly Trp Arg  
                   260                                  265                                  270  
 Gln Leu Leu Gly Leu Leu Pro Glu His Met Ala Glu Lys Leu Cys Glu  
                   275                                  280                                  285  
 Ala Trp Ala Phe Gly Gln Ser His Gln Thr Gly Val Val Ala Leu Gly  
                   290                                  295                                  300  
 Leu Leu Thr Cys Leu Leu Ala Met Leu Leu Ala Gly Arg Ile Arg Leu  
                   305                                  310                                  315                                  320  
 Arg Arg Ile Asp Ala Phe Cys Thr Cys Leu Trp Ala Leu Leu Leu Gly  
                                   325                                  330                                  335

Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro Ser Trp Leu  
 340 345 350

Asn Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu Val Gly Phe  
 355 360 365

Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg Arg Phe Arg  
 370 375 380

Pro Arg Arg Ser Glu Lys Gln Pro  
 385 390

&lt;210&gt; 93

&lt;211&gt; 2203

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 93

cagcgggtggg aggcggcgac cagccgggtg aggccccagg cttggcctca ccacaatgtg 60  
 gcacgaggct cggaagcatg agcggaagct tcgaggcatg atggctcgact acaagaagag 120  
 ggcggagcgg agacgggagt attatgaaa gatcaagaag gacccagccc agttcctgca 180  
 ggtacatggc cgagcttgca aggtgcacct ggattctgca gtcgccttg cgcgtgagag 240  
 ccctgttaat atgatgccct ggcaggggga caccaacaac atgattgacc gattcgatgt 300  
 ccgtgccac ctggaccaca tccccgacta cccccccct ctgctacca ccatctcccc 360  
 agaacaggag tcggacgaac ggaagtgtaa ctacgagcgc tacagaggcc tgggtgcagaa 420  
 cgactttgcc ggcatctcag aggagcagtg cctgtaccag atctacattg atgagttgta 480  
 cggaggcctc cagagaccca gcgaagatga gaagaagaag ctggcagaga agaaggcttc 540  
 catcggttat acctacgagg acagcacggg ggccgaggta gagaaggcgg cagaaaagcc 600  
 agaggaggag gagtacgagg ccgaggagga gagcaactcg gacgaagatg aggtcatccc 660  
 cgacatcgac gtggagggtg acgtggatga attgaaccag gagcagggtg cagatctcaa 720  
 caaacaggcc acgacttatg gcatggccga cggtgacttc gtcaggatgc tccggaaaga 780  
 caaggaggag gcagaggcca tcaagcatgc caaggctctt gaggaggaga aggccatgta 840  
 ctccggagcg cgctctcgac gccagcggag agagtttcgg gagaagcggc tgaggggtcg 900  
 caagatcagc ccacccagct atgcccgcg agacagcccc acctatgacc cctataagcg 960  
 gtcaccctcg gagtccagct cagagtcccg ctcccgctcc cgctccccga ccccgggcgg 1020  
 cgaggagaag atcacgttca tcaccagttt tgggggcagc gatgaggagg cagccgcagc 1080  
 cgctgctgcc gcagcagcat caggagtcac cacagggaag ccccccgcac ctcccagcc 1140  
 tggcggcccc gccccgggac gtaatgccag cgcccgccgc cgctcctct cctcctctc 1200  
 ctctctctct gctctcagga cctccagtc ccgctccagc tctcgtccca gctcccgtc 1260  
 tcgcccgtgt gggggctact accgttccgg ccgccacgcc cgctcccgtt cccgctcctg 1320  
 gtcccgcctc cgctcccgtt cccggcgcta tccccggtcc cgtagccgtg gccggcggca 1380  
 ctcaagggtgg ggctcccag acggacaccg gtactcccgc tcgcccggcc gccgtggtgg 1440  
 ttacggggccc cggcgagaa gcaggagccg ctcccactca ggggaccgct acaggcgggg 1500  
 cggccggggc ctcaaggacc acagcagtag ccgcagccgc agcagctggt cctcagccc 1560  
 gtcccgcagt cgcagcctga ctgcagccg cagccatagc cccagcccca gccagagccg 1620  
 cagccgcagc cgcagccgca gccagagccc ctgcctatca cccgcaagag agaagctgac 1680  
 caggccggcc gctcccctg ctgtgggcga gaagctgaaa aagaccgaac ctgccgctgg 1740  
 taaagagaca ggagctgcca aacccaagct gacgcctcag gagaagctga aactgaggat 1800  
 gcagaaggcg ctgaacaggc agttcaaggc ggataagaag gcggcacaag aaaagatgat 1860  
 ccagcaggag catgagcggc aggagcggga agacgagctt cgagccatgg cccgcaagat 1920  
 ccgcatgaag gagcgggaac gccgagagaa ggagagagaa gagtgggaac gccagtacag 1980  
 ccggcagagc cgctcaccct cccccgata cagtcagaaa tacagctctt ctcaaggcg 2040  
 ctcaagggtc cgatcccga gccccatta ccgacattag gcagaagagt ggggggtggg 2100  
 gaggacaagg ggggtgggtaa ggggtcaag ctgtgatgct gctggtttta tctctagtga 2160  
 aataaagtca aaagtattt aattcccgtc aaaaaaaaaaaa aaa 2203

&lt;210&gt; 94

&lt;211&gt; 674

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 94

Met Trp His Glu Ala Arg Lys His Glu Arg Lys Leu Arg Gly Met Met  
 1 5 10 15  
 Val Asp Tyr Lys Lys Arg Ala Glu Arg Arg Arg Glu Tyr Tyr Glu Lys  
 20 25 30  
 Ile Lys Lys Asp Pro Ala Gln Phe Leu Gln Val His Gly Arg Ala Cys  
 35 40 45  
 Lys Val His Leu Asp Ser Ala Val Ala Leu Ala Ala Glu Ser Pro Val  
 50 55 60  
 Asn Met Met Pro Trp Gln Gly Asp Thr Asn Asn Met Ile Asp Arg Phe  
 65 70 75 80  
 Asp Val Arg Ala His Leu Asp His Ile Pro Asp Tyr Thr Pro Pro Leu  
 85 90 95  
 Leu Thr Thr Ile Ser Pro Glu Gln Glu Ser Asp Glu Arg Lys Cys Asn  
 100 105 110  
 Tyr Glu Arg Tyr Arg Gly Leu Val Gln Asn Asp Phe Ala Gly Ile Ser  
 115 120 125  
 Glu Glu Gln Cys Leu Tyr Gln Ile Tyr Ile Asp Glu Leu Tyr Gly Gly  
 130 135 140  
 Leu Gln Arg Pro Ser Glu Asp Glu Lys Lys Lys Leu Ala Glu Lys Lys  
 145 150 155 160  
 Ala Ser Ile Gly Tyr Thr Tyr Glu Asp Ser Thr Val Ala Glu Val Glu  
 165 170 175  
 Lys Ala Ala Glu Lys Pro Glu Glu Glu Glu Ser Ala Ala Glu Glu Glu  
 180 185 190  
 Ser Asn Ser Asp Glu Asp Glu Val Ile Pro Asp Ile Asp Val Glu Val  
 195 200 205  
 Asp Val Asp Glu Leu Asn Gln Glu Gln Val Ala Asp Leu Asn Lys Gln  
 210 215 220  
 Ala Thr Thr Tyr Gly Met Ala Asp Gly Asp Phe Val Arg Met Leu Arg  
 225 230 235 240  
 Lys Asp Lys Glu Glu Ala Glu Ala Ile Lys His Ala Lys Ala Leu Glu  
 245 250 255  
 Glu Glu Lys Ala Met Tyr Ser Gly Arg Arg Ser Arg Arg Gln Arg Arg  
 260 265 270  
 Glu Phe Arg Glu Lys Arg Leu Arg Gly Arg Lys Ile Ser Pro Pro Ser  
 275 280 285  
 Tyr Ala Arg Arg Asp Ser Pro Thr Tyr Asp Pro Tyr Lys Arg Ser Pro  
 290 295 300

Ser Glu Ser Ser Ser Glu Ser Arg Ser Arg Ser Arg Ser Pro Thr Pro  
 305 310 315 320  
 Gly Arg Glu Glu Lys Ile Thr Phe Ile Thr Ser Phe Gly Gly Ser Asp  
 325 330 335  
 Glu Glu Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ser Gly Val Thr  
 340 345 350  
 Thr Gly Lys Pro Pro Ala Pro Pro Gln Pro Gly Gly Pro Ala Pro Gly  
 355 360 365  
 Arg Asn Ala Ser Ala Arg Arg Arg Ser Ser Ser Ser Ser Ser Ser  
 370 375 380  
 Ser Ala Ser Arg Thr Ser Ser Ser Arg Ser Ser Ser Arg Ser Ser Ser  
 385 390 395 400  
 Arg Ser Arg Arg Gly Gly Tyr Tyr Arg Ser Gly Arg His Ala Arg  
 405 410 415  
 Ser Arg Ser Arg Ser Trp Ser Arg Ser Arg Ser Arg Ser Arg Arg Tyr  
 420 425 430  
 Ser Arg Ser Arg Ser Arg Gly Arg Arg His Ser Gly Gly Gly Ser Arg  
 435 440 445  
 Asp Gly His Arg Tyr Ser Arg Ser Pro Ala Arg Arg Gly Gly Tyr Gly  
 450 455 460  
 Pro Arg Arg Arg Ser Arg Ser Arg Ser His Ser Gly Asp Arg Tyr Arg  
 465 470 475 480  
 Arg Gly Gly Arg Gly Leu Arg His His Ser Ser Ser Arg Ser Arg Ser  
 485 490 495  
 Ser Trp Ser Leu Ser Pro Ser Arg Ser Arg Ser Leu Thr Arg Ser Arg  
 500 505 510  
 Ser His Ser Pro Ser Pro Ser Gln Ser Arg Ser Arg Ser Arg Ser Arg  
 515 520 525  
 Ser Gln Ser Pro Ser Pro Ser Pro Ala Arg Glu Lys Leu Thr Arg Pro  
 530 535 540  
 Ala Ala Ser Pro Ala Val Gly Glu Lys Leu Lys Lys Thr Glu Pro Ala  
 545 550 555 560  
 Ala Gly Lys Glu Thr Gly Ala Ala Lys Pro Lys Leu Thr Pro Gln Glu  
 565 570 575  
 Lys Leu Lys Leu Arg Met Gln Lys Ala Leu Asn Arg Gln Phe Lys Ala  
 580 585 590  
 Asp Lys Lys Ala Ala Gln Glu Lys Met Ile Gln Gln Glu His Glu Arg  
 595 600 605  
 Gln Glu Arg Glu Asp Glu Leu Arg Ala Met Ala Arg Lys Ile Arg Met  
 610 615 620

Lys Glu Arg Glu Arg Arg Glu Lys Glu Arg Glu Glu Trp Glu Arg Gln  
 625 630 635 640

Tyr Ser Arg Gln Ser Arg Ser Pro Ser Pro Arg Tyr Ser Arg Glu Tyr  
 645 650 655

Ser Ser Ser Arg Arg Arg Ser Arg Ser Arg Ser Arg Ser Pro His Tyr  
 660 665 670

Arg His

<210> 95

<211> 1014

<212> DNA

<213> Homo sapiens

<400> 95

```

gggcgcgcgc gcctcctcct ccattggctgt ttaccggcgt gcattgtggg agtttgacct 60
ccgccgcgcgc caaccgcgcgc ctcagcttgc gccgcgcgcgc ccgccgcgcgc cgccgcgcac 120
gccatgggag ccgtgactga cgacgaagtt atacggaagc gtctcctcat tgatggagat 180
ggtgctggag atgatcggag aattaatctg ctagtgaaga gtttcattaa atggtgcaac 240
tctgggtccc aggaagaggg atatatgccag taccaacgta tgctgagcac gctgtctcaa 300
tgtgaatttt caatgggcaa aactttacta gtatatgata tgaatctcag agaaatggaa 360
aattatgaaa aaatttacia ggaaatagaa tgtagcatag ctggagcaca tgaaaaaatt 420
gctgagtgcg aaaagcaa atcttcaagca aaacgaatac gaaaaaatcg ccaagaatat 480
gatgctttgg caaaagtgat tcagcaccat ccagacaggc atgagacatt aaaggaacta 540
gaggtctctg gaaaagaatt agagcatctt tcacacatta aagaaagtgt tgaagataag 600
ctggaattga gacggaaaca gtttcatgtt cttcttagta ccattcatga acttcagcaa 660
acattggaaa atgatgaaa actctcagag gtagaagaag ctcaggaagc aagcatggaa 720
acagatccta agccatagac aggctaattg cccaccactc ccaggaatat tgaatatagct 780
acatgaccat aatgtgttta aaatgtggta tgctcttgag atatttaaag ttttggcagt 840
aaaatactct gtttttaagt atgaatgtat ttcattcata tttcctctca caaaggaaaa 900
tgacttcagt atagatttgt ttttattaaa atgcattttt tattcttaag tggtaggaag 960
caacatccaa aaatgcttaa taaaatgctt ttaagctgca aaaaaaaaaa aaaa 1014

```

<210> 96

<211> 204

<212> PRT

<213> Homo sapiens

<400> 96

```

Met Gly Ala Val Thr Asp Asp Glu Val Ile Arg Lys Arg Leu Leu Ile
  1 5 10 15

Asp Gly Asp Gly Ala Gly Asp Asp Arg Arg Ile Asn Leu Leu Val Lys
  20 25 30

Ser Phe Ile Lys Trp Cys Asn Ser Gly Ser Gln Glu Glu Gly Tyr Ser
  35 40 45

Gln Tyr Gln Arg Met Leu Ser Thr Leu Ser Gln Cys Glu Phe Ser Met
  50 55 60

Gly Lys Thr Leu Leu Val Tyr Asp Met Asn Leu Arg Glu Met Glu Asn
  65 70 75 80

Tyr Glu Lys Ile Tyr Lys Glu Ile Glu Cys Ser Ile Ala Gly Ala His
  85 90 95

```



Glu Lys Ile Ala Glu Cys Lys Lys Gln Ile Leu Gln Ala Lys Arg Ile  
 100 105 110  
 Arg Lys Asn Arg Gln Glu Tyr Asp Ala Leu Ala Lys Val Ile Gln His  
 115 120 125  
 His Pro Asp Arg His Glu Thr Leu Lys Glu Leu Glu Ala Leu Gly Lys  
 130 135 140  
 Glu Leu Glu His Leu Ser His Ile Lys Glu Ser Val Glu Asp Lys Leu  
 145 150 155 160  
 Glu Leu Arg Arg Lys Gln Phe His Val Leu Leu Ser Thr Ile His Glu  
 165 170 175  
 Leu Gln Gln Thr Leu Glu Asn Asp Glu Lys Leu Ser Glu Val Glu Glu  
 180 185 190  
 Ala Gln Glu Ala Ser Met Glu Thr Asp Pro Lys Pro  
 195 200

<210> 97  
 <211> 955  
 <212> DNA  
 <213> Homo sapiens

<400> 97  
 aatcctcaac aaaatagtag caaaacaaat ccaatagtag atcacgaaga taatacagta 60  
 tgatcaaagtg ggatttattt caaggatgca tagatgattc aacattcacg atcaataaaa 120  
 tttattctgt taatttttca taaggatgtg ttttaaataa gaatgggtatt gtatattaga 180  
 cataaaatga ctgttttagt tagcattctt agagctagct tcataatcca attaatatac 240  
 ttgcaacttg agtgcagggtg ttttaatttt tataactgta tcctgtatgc tattcaaagtg 300  
 agctaattgt agttattctt ataccatttg gtattgggtt ccatagtata cataagtttt 360  
 atttttgttt ttctgttagt accttcaa atttactttc catagtttct ctggcataaa 420  
 agctcccagt ttctatcttc aacagttcag gtcttgggat atctatcgtt ttatttggtt 480  
 ttataacttt tatttagaag agttacatcc ttttttagctt atttaatgat aaaaagtcca 540  
 ctttttccac ttttgatttt gaatgaattg ctgcccctaa catggatcta tcttggtttt 600  
 acagagagaa gagaagagga agatattgaa gagaagaaat cgattaagaa aaaaattaaa 660  
 gaacttaagt ttttagattc taaaattgcc cagaaccttt gtaagtatca tattccaata 720  
 ccattcaagg acagtggaaa ttttctttaa aatgatttca ttttctttaa gaccgattat 780  
 tcattatttg ctattttcat tttgttatta tatgcatgat aaattcacag ataactctcc 840  
 tttagggtaaa ttatgggatt aaatgcttca aaagataagt gcatattaga aaatacaaat 900  
 aagaagaggt tttaaaatga aattctacct ttcataactg aaaaaaaaaa aaaaa 955

<210> 98  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 98  
 Met Ile Lys Ser Ser Leu Phe Pro Leu Leu Tyr Leu Asn Glu Leu Leu  
 1 5 10 15  
 Pro Leu Thr Trp Ile Tyr Leu Gly Phe Thr Glu Arg Arg Glu Glu Glu  
 20 25 30  
 Asp Ile Glu Glu Lys Lys Ser Ile Lys Lys Lys Ile Lys Glu Leu Lys  
 35 40 45

Phe Leu Asp Ser Lys Ile Ala Gln Asn Leu Cys Lys Tyr His Ile Pro  
 50 55 60

Ile Pro Phe Lys Asp Ser Gly Asn Ile Ser Leu Asn Asp Phe Ile Phe  
 65 70 75 80

Phe Lys Thr Asp Tyr Ser Leu Phe Ala Ile Phe Ile Leu Leu Leu Tyr  
 85 90 95

Ala

<210> 99  
 <211> 1375  
 <212> DNA  
 <213> Homo sapiens

<400> 99  
 gtcttctttt agggagcagg agtgcactctg gtaattgagg gtggatgttg tgtgtgctgg 60  
 ggaggggtcc ttctgtttgg tgctaccctt gtctactctg cccctggatg gtgcgggggtg 120  
 ctttctccac cccacactc cctgctcagc tctctgtgct gccctgcatg cccaggcttg 180  
 tgagccaagc tgcttttttg ggcaggaggt agcagcaggt gggaggggtt acccatcagc 240  
 ccttgcaagt cccccactca ggctcttgga aggtccaggg atgggctctg atgagagggg 300  
 aaaagatgct cagggaaaca caggcctcag ctgcctagag gaccctcccc ctgccttgca 360  
 gtgggctcgg gtagagcagt atcaggagct aggggtgtct gctgcccaca ctctgtcttt 420  
 ttgggatatc taactgctaa ggagggaggt gacatcccc ttctggctca tgtgtctgac 480  
 accaacaaca tgggtctctgt cctctctctt ttgactctcc ctttgtcctc cccatagagc 540  
 tggggtgggg tggatcccta tacctggggc aggcagcccc aaagtggggg agggggatgg 600  
 cagagactgt aaaggcgcca ctggactctg gcaaggcctt tattaccttt actccccctc 660  
 ctctcccatc accagctca aggcctgagg ggtgcagggg ctcttgccag ctactgggtg 720  
 aggtttctctg gcacagactc acccttcttt ctggcaccac ctcttccct tttgaagaga 780  
 cagcaacagc cgtagcaaaa gcagctgctg ctctgtctat gaggggtgat atatttttta 840  
 cccaaagctc tggaattgta catttatttt ttaaaactca aagagggaaa gaggccttgta 900  
 tcatatgtga acattgtatc ataggtaatg ttgtacagac ctttttatac agtgatctgt 960  
 cttgttctctg cagcaaaaat cctctatgga cataggaggt gctgtgtccc atgccctctt 1020  
 gccctgacag tgtcccatgg gcccccttct gctccctgcc cctccctgc tactgctgat 1080  
 gcactctcct ctccctgcag cccctggctt cccagccttc ctctgacctt ctccaacag 1140  
 ccttggaact ccagctgcca ccacctctg ggtcgacac tgggacccac tggcccagtc 1200  
 ttggctgctg cttacccta gccttgatgc ctgcccaggg acccccagcc cctcccggtt 1260  
 gccctgcagc tttaacagag tgaaccatgt gtattgtaca ggcgcggttg tcattgcaga 1320  
 aaccgctggg tggagaagaa gccgataaag tctatgaatc aaaaaaaaaa aaaaa 1375

<210> 100  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

<400> 100  
 Met Ala Glu Thr Val Lys Ala Pro Leu Asp Ser Gly Lys Ala Phe Ile  
 1 5 10 15

Thr Phe Thr Pro Leu Pro Leu Pro Ser Pro Ala Ser Arg Pro Glu Gly  
 20 25 30

Cys Arg Gly Ser Trp Gln Leu Leu Gly Glu Val Ser Trp His Arg Leu  
 35 40 45

Thr Leu Leu Ser Gly Thr Thr Ser Phe Pro Phe Glu Glu Thr Ala Thr

50

55

60

Ala Val Ala Lys Ala Ala Ala Ala Pro Ala Met Arg Val Tyr Ile Phe  
65 70 75 80

Phe Thr Gln Ser Ser Gly Ile Val His Leu Phe Phe Lys Thr Gln Arg  
85 90 95

Gly Lys Glu Pro Cys Ile Ile Cys Glu His Cys Ile Ile Gly Asn Val  
100 105 110

Val Gln Thr Leu Leu Tyr Ser Asp Leu Ser Cys Ser Cys Ser Lys Asn  
115 120 125

Pro Leu Trp Thr  
130

&lt;210&gt; 101

&lt;211&gt; 1213

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 101

ggcttcagggt tgaagtcctt gggtcttcca gttcctcagc gggttaggtag gggctcctgc 60  
atcaccttca gaatccagtt ccaaccccca ctctccttag gccttgtgct ctgctctgcc 120  
ctgccagggt gcccttgtcc atgtgagtag catgggcggg tgggtggggac ggcagtgggtg 180  
atgaaggggg tgcaccacag gcctcatgaa gcagttccca catgggcgtg tggctggggc 240  
gtggccacca cagagcacat ggctgtgtct aggcgcaagc actttagcag tatctgttta 300  
catgcgcaag gatcaagcg actacctgtg ctgtctactg ggacagcagt ctccgagcta 360  
ctccgtacct cctctgcca ggtcgtggag ttaggcccc gtcctactt gtcactggtt 420  
cccactgtgc tctaactgt gcagcacctg ggagctctg cctggggctg gaggccctgg 480  
taggagctgc agttggaggc cgttctgtgc ccagcagcgg tgagcggctc ccatgggccc 540  
tgtgtctgca gggagccagg gctgcggcac atgtgctgtg aaactggcac ccacctggcg 600  
tgctgctgcc gccactgct tctgcagca cctcctaccc tgctccgtgt cctccctctc 660  
cccgcgcctg gctcaggagt gctggaaaag ctcacgcctc ggcctgggag cctggcctct 720  
tgatatacct cgagcttccc ctgtgctccc cagccccagg accactggcc cctgggcctg 780  
aggggctggg ggccccacga cctgcagcgt cgagtccggg agagagcccg gagcggcgtg 840  
ccatctcggc tcggccttgc tgagagcctc cgccctggct ttctccctgt ctggattcag 900  
tggctcacgt tgggtgctaca cagctagaat agatatatt agagagagag atatttttaa 960  
gacaaagccc acaattagct gtcctttaac accgcagaac cccctcccag aagaagagcg 1020  
atccctcgga cgggtccggg gggcacccctc agccgggctc tttgcagaag cagcaccgt 1080  
gactgtggg cgggcctca gatgtgtaca tatacggcta tttctattt tactgttctt 1140  
cagatttagt acttgtaaata aaacacacac attaggaga gattaaacat ttttgctaaa 1200  
aaaaaaaaaaa aaa 1213

&lt;210&gt; 102

&lt;211&gt; 100

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 102

Met Lys Gly Val His His Arg Pro His Glu Ala Val Pro Thr Trp Ala  
1 5 10 15

Cys Gly Trp Gly Val Ala Thr Thr Glu His Met Ala Val Ser Arg Arg  
20 25 30

Lys His Phe Ser Ser Ile Cys Leu His Ala Gln Gly Ser Ser Arg Leu  
35 40 45

Pro Val Leu Ser Thr Gly Thr Ala Val Ser Glu Leu Leu Arg Thr Ser  
 50 55 60

Leu Cys Gln Val Val Glu Leu Gly Pro Ser Pro Tyr Leu Ser Leu Val  
 65 70 75 80

Pro Thr Val Leu Leu Thr Val Gln His Leu Gly Ala Leu Ala Trp Gly  
 85 90 95

Trp Arg Pro Trp  
 100

<210> 103

<211> 1036

<212> DNA

<213> Homo sapiens

<400> 103

cctcaaatgc tttctttctt cagatgcttt ttcgtgtaca tgatactagt agacactttt 60  
 ctcttttatat ttactgatat tgaaaatcat acgcaataaa atattgatgt ttgaaggcag 120  
 tggtcaccaa ttgggttaaaa aactatgaaa tgtaaactga attggtatat ctctatcctt 180  
 tttgcttttc tctgtgtttt taatgtatgg aataaatctc ataaatagaa agaaaaataa 240  
 tctagaaatt tttcaaagct agtactcttt ctcttataa atgtacacaa ttttaatctt 300  
 tttacaaatt tatttaactg tacctactgt acttattgta gattcaatga cgcagttaag 360  
 tcatcaccca aggatttatg aatttgagat tactgacctg ttttcttcat attgcattca 420  
 catcaatatt tgtgaatttg ttgttcagct tttcattcaa acaaaaaata ttccctcaag 480  
 aaagctccat ttttatcata aacatttcaa cataaccaac attagaacaa gtctgccatg 540  
 ttaaaaaataa tttaaagact tatctctgaa aacgggtatcc agaaacgcag gtgttcccag 600  
 taatgtagct tcaaaaaataa aatgtgctat ttatatgaca tgaaattcat aacttttggg 660  
 aggggtatatt tatgacagca taaaaataa attctgtgct ataaagaaga tccaacaaat 720  
 taaccatata agcacagaaa atagagaaac acagttattg aatctactct tgcattaac 780  
 attttcaaaa aacaaaatgc atattgtaat atttggtaca tgacacttgc atgttgatat 840  
 gcctatatac ttacaaagta ttcaatgtgt acttagcggc gcttaaaata tgtcatgtac 900  
 aactcttata aacattttta cagggttccc atttgcactt catctttcag taaagtcttg 960  
 tcagaaaaaaa attgtctgat aaatatggaa aaataaaatt tgaattttag ttaaaaaaaa 1020  
 aaaaaaaaaa aaaaaa 1036

<210> 104

<211> 87

<212> PRT

<213> Homo sapiens

<400> 104

Met Tyr Thr Ile Leu Ile Phe Leu Gln Ile Tyr Leu Thr Val Pro Thr  
 1 5 10 15

Val Leu Ile Val Asp Ser Met Thr Gln Leu Ser His His Pro Arg Ile  
 20 25 30

Tyr Glu Phe Glu Ile Thr Asp Leu Phe Ser Ser Tyr Cys Ile His Ile  
 35 40 45

Asn Ile Cys Glu Phe Val Val Gln Leu Phe Ile Gln Thr Lys Asn Ile  
 50 55 60

Pro Ser Arg Lys Leu His Phe Tyr His Lys His Phe Asn Ile Thr Asn  
 65 70 75 80

Ile Arg Thr Ser Leu Pro Cys

85

&lt;210&gt; 105

&lt;211&gt; 2349

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 105

```

tttttttttt ttttttgatt cttggtaaaa ttttatccaa aaaacaggat acatatatat 60
ttagagaagg aaatatgaaa tcaagagttt tggcagcccc tgcttttttt ttttttttag 120
ctccctaaag actgtagcag gataaaagga tcaactggctc cgagtctctt tgagataaca 180
agtgtatgaaa taaaaaagaa agcccatacc ctcaaataag gtcaggtaac cccattgccc 240
accctcccta caaggtaaaa aatgagtact tttagtaaca gttcagaatt catctttatc 300
tcctacctgc ctcatcgggtg gaagtttaaa gtcatgattt tttttagaca ttgatacttg 360
tgtctataga caaataaact catattagac ggccaaagag gcctaccact gctgcaccag 420
cagtatacct cagcactgc ctcaccactg cccctgcgcc cagatgctcc tgttgaaaag 480
tcacccgagg agacagctac ccaggctccc agtctggaga gtctgacttt aaagctagag 540
cagcaggttg tggccaggag ccgaccaacc ccacaagact atgagatgag agtatcccc 600
tctgatacta cccctctggt ttcccgaggt gttccaccag tcaaactgga ggatgaggat 660
gattcggact ctgagctgga cttgagcaag ctgtcaccat cttctctctc ttctcatcc 720
tcattccagct ccagctccag cactgatgag agtgaggatg agaaggaaga gaagctaact 780
gaccagtccc gctcaaagct ctatgatgaa gagagtctcc tgtccctcac tatgtcccaa 840
gatggattcc caaatgaaga tggagaacaa atgacccctg agcttctgct actgcaggaa 900
agacaaagag cctctgagtg gcccaggat cgtgtcctga taaaccgtat tgacctcgtc 960
tgccaggctg tactctcagg gaagtggcct tctagccgta ggagccagga aatggtaaca 1020
ggaggaatth tggggccagg caaccacttg ctagacagtc cctcattgac tcctggagaa 1080
tatggtgact ctccagtcac cacaccacga agtagtagtg cagcttccat ggcagaggag 1140
gaagcatctg cagtcagcac agcggcagcc cagttcacca aacttcgccg aggcattgat 1200
gaaaaggagt ttacagttca aatcaaagat gaggaaggat tgaagttaac attccagaag 1260
cacaagttga tggcgaatgg agtaatggga gatggacatc cactgtttca taagaagaag 1320
gggaacagaa agaagctagt agagctggag gtggagtgcg tggaaagagcc taatcacctt 1380
gatgtggacc tggagaccgg gatccctgtc atcaataagg tggatggtag ttgtctggtg 1440
ggtgaggatg cccctcgcgg ggctgaactg gagatgtggt tacaggggtc tccagagttt 1500
gctgttgatc cccgatttct agcgtatatg gaggatcgca gaaaacagaa gtggcaaaaga 1560
tgtaaaaaaa ataataaggc agaattgaac tgtttgggaa tggaaaccagt acagacagct 1620
aactctagaa atgggaaaaa gggatcatcac actgaaacgg tgttcaaccg ggttttgcca 1680
gggcctattg caccagagag cagcaagaag cgggcccgtg ggatgcgacc agacctttct 1740
aagatgatgg ccctcatgca ggggtggaag actgggtctc tatctctgca taacacgttc 1800
caacacagca gtagtggcct acagtctgtg tcattcttgg gtcacagcag tgccacttct 1860
gcatctttgc cttttatgcc atttgtgatg ggtgggtgcac catcatcccc tcatgtagac 1920
tccagcacca tgcttcatca ccaccaccac caccaccacc cccaccatca ccaccatcac 1980
catccaggct tgagagcccc tggctacccc tcttcaccag tgactaccgc ctctgggtact 2040
accttgcggt tgccaccact gcaacctgag gaggatgacg atgaggatga agaagatgat 2100
gatgacttat ctcagggcta tgatagctca gaaagggact tctcactcat tgatgatcct 2160
atgatgccag ctaactcaga ctccagtga gatgctgatg actgaagccc cagcatgggc 2220
cccattgctt gggcggtgc tgtattttca tttactctgg cccttggact atggaaacgt 2280
gggaggggca ggggagatgt ggggaagtcc aggactccag gaggtgaaaa ggaaaaaaa 2340
aaaaaaa

```

2349

&lt;210&gt; 106

&lt;211&gt; 539

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 106

```

Met Arg Val Ser Pro Ser Asp Thr Thr Pro Leu Val Ser Arg Ser Val
  1                      5                      10                      15

```

Pro Pro Val Lys Leu Glu Asp Glu Asp Asp Ser Asp Ser Glu Leu Asp  
                   20                                  25                                  30  
 Leu Ser Lys Leu Ser Pro Ser Ser Ser Ser Ser Ser Ser Ser Ser  
                   35                                  40                                  45  
 Ser Ser Ser Ser Thr Asp Glu Ser Glu Asp Glu Lys Glu Glu Lys Leu  
                   50                                  55                                  60  
 Thr Asp Gln Ser Arg Ser Lys Leu Tyr Asp Glu Glu Ser Leu Leu Ser  
                   65                                  70                                  75                                  80  
 Leu Thr Met Ser Gln Asp Gly Phe Pro Asn Glu Asp Gly Glu Gln Met  
                   85                                  90                                  95  
 Thr Pro Glu Leu Leu Leu Leu Gln Glu Arg Gln Arg Ala Ser Glu Trp  
                   100                                  105                                  110  
 Pro Lys Asp Arg Val Leu Ile Asn Arg Ile Asp Leu Val Cys Gln Ala  
                   115                                  120                                  125  
 Val Leu Ser Gly Lys Trp Pro Ser Ser Arg Arg Ser Gln Glu Met Val  
                   130                                  135                                  140  
 Thr Gly Gly Ile Leu Gly Pro Gly Asn His Leu Leu Asp Ser Pro Ser  
                   145                                  150                                  155                                  160  
 Leu Thr Pro Gly Glu Tyr Gly Asp Ser Pro Val Pro Thr Pro Arg Ser  
                   165                                  170                                  175  
 Ser Ser Ala Ala Ser Met Ala Glu Glu Glu Ala Ser Ala Val Ser Thr  
                   180                                  185                                  190  
 Ala Ala Ala Gln Phe Thr Lys Leu Arg Arg Gly Met Asp Glu Lys Glu  
                   195                                  200                                  205  
 Phe Thr Val Gln Ile Lys Asp Glu Glu Gly Leu Lys Leu Thr Phe Gln  
                   210                                  215                                  220  
 Lys His Lys Leu Met Ala Asn Gly Val Met Gly Asp Gly His Pro Leu  
                   225                                  230                                  235                                  240  
 Phe His Lys Lys Lys Gly Asn Arg Lys Lys Leu Val Glu Leu Glu Val  
                   245                                  250                                  255  
 Glu Cys Met Glu Glu Pro Asn His Leu Asp Val Asp Leu Glu Thr Arg  
                   260                                  265                                  270  
 Ile Pro Val Ile Asn Lys Val Asp Gly Thr Leu Leu Val Gly Glu Asp  
                   275                                  280                                  285  
 Ala Pro Arg Arg Ala Glu Leu Glu Met Trp Leu Gln Gly His Pro Glu  
                   290                                  295                                  300  
 Phe Ala Val Asp Pro Arg Phe Leu Ala Tyr Met Glu Asp Arg Arg Lys  
                   305                                  310                                  315                                  320  
 Gln Lys Trp Gln Arg Cys Lys Lys Asn Asn Lys Ala Glu Leu Asn Cys  
                   325                                  330                                  335

Leu Gly Met Glu Pro Val Gln Thr Ala Asn Ser Arg Asn Gly Lys Lys  
 340 345 350  
 Gly His His Thr Glu Thr Val Phe Asn Arg Val Leu Pro Gly Pro Ile  
 355 360 365  
 Ala Pro Glu Ser Ser Lys Lys Arg Ala Arg Arg Met Arg Pro Asp Leu  
 370 375 380  
 Ser Lys Met Met Ala Leu Met Gln Gly Gly Ser Thr Gly Ser Leu Ser  
 385 390 395 400  
 Leu His Asn Thr Phe Gln His Ser Ser Ser Gly Leu Gln Ser Val Ser  
 405 410 415  
 Ser Leu Gly His Ser Ser Ala Thr Ser Ala Ser Leu Pro Phe Met Pro  
 420 425 430  
 Phe Val Met Gly Gly Ala Pro Ser Ser Pro His Val Asp Ser Ser Thr  
 435 440 445  
 Met Leu His His His His His His Pro His Pro His His His His His  
 450 455 460  
 His His Pro Gly Leu Arg Ala Pro Gly Tyr Pro Ser Ser Pro Val Thr  
 465 470 475 480  
 Thr Ala Ser Gly Thr Thr Leu Arg Leu Pro Pro Leu Gln Pro Glu Glu  
 485 490 495  
 Asp Asp Asp Glu Asp Glu Glu Asp Asp Asp Asp Leu Ser Gln Gly Tyr  
 500 505 510  
 Asp Ser Ser Glu Arg Asp Phe Ser Leu Ile Asp Asp Pro Met Met Pro  
 515 520 525  
 Ala Asn Ser Asp Ser Ser Glu Asp Ala Asp Asp  
 530 535

&lt;210&gt; 107

&lt;211&gt; 3004

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 107

ggggcatgag catctcaggg ctgccagaat ggcttttgcg gagtgcatag caccagcgtg 60  
 tgtcatgtct tggctgcgtt tctggggccc atggcccctc cttacgtggc aactattgtc 120  
 tttactagtc aaggaggctc agcctctggt gtgggtcaag gaccgctcc agctgacctc 180  
 taacccctcg gggccacctg agccctggtc ttcccgctcc tcccatctcc catgggaatc 240  
 tccccatgca cctgctcccc cagcagcccc gggggacttt gattacctgg ggccctctgc 300  
 ttcttcgcag atgtcagccc tgcctcagga accaactgaa aatttggctc cattcttgaa 360  
 ggaattggat tcagctggag agctgcccct ggggcccagag ccgttcttgg ctgcacatca 420  
 ggacttaaat gacaagcggg ctccagaaga aaggctccca gaggtgggtc cgcttctcaa 480  
 ccgggatcag aaccaggccc tagttcagct tcctcgccctc aagtgggttc aaactacaga 540  
 tctagatcgg gctgcaggtc atcaggcaga tgaataactt gttccactag acagtaaggt 600  
 ttcaagacca accaaatttg ttgtttcgcc caagaacctg aagaaagatc tagctgaacg 660  
 ttggagcctt cctgagattg ttgggattcc acaccaatta tccaaacctc agcgtcagaa 720  
 acagactttg ccagatgatt atttgagtat ggacacactg tatcccgga gcctacctcc 780  
 agaactccgg gtgaacgcag atgagcctcc agggcctcct gagcaagttg gactttctca 840

```

attccatcta gagcccaaaa gtcaaaatcc agagaccctt gaagacatcc agtcctcttc 900
actccaggaa gaagccccag cgcagcttct acagctccct caggaggtag aaccttcaac 960
ccagcaggag gccccagctc tgctccaga gtctctatg gagagtctag ctcaaactcc 1020
actgaatcat gaagtgcacag ttcaacctcc aggtgaggat caagctcatt ataatttgc 1080
caagtttaca gtcaaacctg cagatgtgga ggttaccatg acttcagagc ctaaaaatga 1140
gacagaatct acccaagccc agcaggaggc cccaattcag cctcccaggg agggcggaacc 1200
ttcttctaca gccctgagga ctacagatcc tctccagaa caccctgagg tgacacttcc 1260
accttcagac aagggtcagg ctacagatcc acacctgact gaagccacag ttcaacctct 1320
ggacctggag cttagcataa ctacagagcc tactacagag gttaaaccgt ctccaaccac 1380
ggaggaaacc tcagctcagc ctccagaccc ggggcttgcc ataactccag aacctactac 1440
agagattgga cattccacag ccctggagaa gactagagct cctcatccag accagggttca 1500
gactctgcat cgaagcctga ctgaagtcac aggtccacct acaaagttag aatcttcgca 1560
ggattcattg gtgcagtctg aaactgcacc agaggaacag aaggcctcca caagcaccaa 1620
catatgtgag ctctgcacct gcggagatga gactctgtca tgtgttggtc tcagcccaa 1680
gcagaggctc cgccaagtgc ctgtgccaga gcccgacacc tacaatggca tcttcaccac 1740
cttaaatctc caaggaaact atatttcata ccttgatgga aatgtatgga aagcatacag 1800
ttggaccgag aaactaatcc tcagtgaata ttatttgact gaattacctt aggtattcatt 1860
tgaaggcctg ctatacctcc agtattttaga tttatcctgc aataaaatac gatatttga 1920
aagacaaaca ttgaatcac taccattttt gcagtatata aatctgggct gcaattttaa 1980
tacaaaactg agccttgga ctttcaggc ctggcacgga atgcagtttt tacacaactt 2040
aatttcaat cgcaatcctc tgactactgt cgaagatcca tatctcttg aactgccggc 2100
attaaaaat ctacagatgg gaacaacaca catcacactt acaacactta agaacttct 2160
cacgatgact gttgaactgg aaaaactgat cttacctagc catatggcct gctgcctctg 2220
ccaattttaa aatagcattg aggtgtctg caagacagtc aagctgcatt gcaacactgc 2280
atgtctgact aacagcatac attgtcctga agaagcatct gtagggaatc cagaaggagc 2340
gttcatgaag atgttacaag cccggaagca gcacatgagc actcagctga ctattgagtc 2400
ggaggcgccc tcagacagca gtggcatcaa cttgtcaggc tttgggggtg atcagcttga 2460
aattcagcta accgagcagc tacggtccct catccccaac gaggatgtga gaaagtcat 2520
gtctcatggt atccggacct tgaaaatgga atgttcagaa acacatgtgc aaggagctg 2580
tgccaagctc atgtcgcgaa caggcctcct cgaagctt ctcagcgagc agcaggaagc 2640
aaaggcattg aatgtagaat gggatacgga ccaacaaaaa acaaattata ttaatgagaa 2700
catggaacag aatgaacaga aagagcagaa gtcaagttag ctcatgaaag aagttccagg 2760
agatgactat aagaacaaac tcatcttcgc aatatctgtg actgtaatac taataatttt 2820
gattataatt ttttgtctta tagaggtgaa ttcacataaa agggcatcag aaaaatacaa 2880
agacaaccca tcaatatcag gagcctgagc atgaggttaa gcatgtggat ggcttgagc 2940
tatgttttta aaattgttat taaatattgg ttttttactt aaaaaaaaaa aaaaaaaaaa 3000
aaaa
3004

```

&lt;210&gt; 108

&lt;211&gt; 959

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 108

```

Met Ala Phe Ala Glu Cys Ile Ala Pro Ala Cys Val Met Ser Trp Leu
  1             5             10             15

```

```

Arg Phe Trp Gly Pro Trp Pro Leu Leu Thr Trp Gln Leu Leu Ser Leu
      20             25             30

```

```

Leu Val Lys Glu Ala Gln Pro Leu Val Trp Val Lys Asp Pro Leu Gln
      35             40             45

```

```

Leu Thr Ser Asn Pro Leu Gly Pro Pro Glu Pro Trp Ser Ser Arg Ser
      50             55             60

```

```

Ser His Leu Pro Trp Glu Ser Pro His Ala Pro Ala Pro Pro Ala Ala
      65             70             75             80

```

```

Pro Gly Asp Phe Asp Tyr Leu Gly Pro Ser Ala Ser Ser Gln Met Ser

```



85	90	95
Ala Leu Pro Gln Glu Pro Thr Glu Asn Leu Ala Pro Phe Leu Lys Glu 100 105 110		
Leu Asp Ser Ala Gly Glu Leu Pro Leu Gly Pro Glu Pro Phe Leu Ala 115 120 125		
Ala His Gln Asp Leu Asn Asp Lys Arg Thr Pro Glu Glu Arg Leu Pro 130 135 140		
Glu Val Val Pro Leu Leu Asn Arg Asp Gln Asn Gln Ala Leu Val Gln 145 150 155 160		
Leu Pro Arg Leu Lys Trp Val Gln Thr Thr Asp Leu Asp Arg Ala Ala 165 170 175		
Gly His Gln Ala Asp Glu Ile Leu Val Pro Leu Asp Ser Lys Val Ser 180 185 190		
Arg Pro Thr Lys Phe Val Val Ser Pro Lys Asn Leu Lys Lys Asp Leu 195 200 205		
Ala Glu Arg Trp Ser Leu Pro Glu Ile Val Gly Ile Pro His Gln Leu 210 215 220		
Ser Lys Pro Gln Arg Gln Lys Gln Thr Leu Pro Asp Asp Tyr Leu Ser 225 230 235 240		
Met Asp Thr Leu Tyr Pro Gly Ser Leu Pro Pro Glu Leu Arg Val Asn 245 250 255		
Ala Asp Glu Pro Pro Gly Pro Pro Glu Gln Val Gly Leu Ser Gln Phe 260 265 270		
His Leu Glu Pro Lys Ser Gln Asn Pro Glu Thr Leu Glu Asp Ile Gln 275 280 285		
Ser Ser Ser Leu Gln Glu Glu Ala Pro Ala Gln Leu Leu Gln Leu Pro 290 295 300		
Gln Glu Val Glu Pro Ser Thr Gln Gln Glu Ala Pro Ala Leu Pro Pro 305 310 315 320		
Glu Ser Ser Met Glu Ser Leu Ala Gln Thr Pro Leu Asn His Glu Val 325 330 335		
Thr Val Gln Pro Pro Gly Glu Asp Gln Ala His Tyr Asn Leu Pro Lys 340 345 350		
Phe Thr Val Lys Pro Ala Asp Val Glu Val Thr Met Thr Ser Glu Pro 355 360 365		
Lys Asn Glu Thr Glu Ser Thr Gln Ala Gln Gln Glu Ala Pro Ile Gln 370 375 380		
Pro Pro Glu Glu Ala Glu Pro Ser Ser Thr Ala Leu Arg Thr Thr Asp 385 390 395 400		
Pro Pro Pro Glu His Pro Glu Val Thr Leu Pro Pro Ser Asp Lys Gly		

101

725	730	735
Ile Glu Ala Val Cys Lys Thr Val Lys Leu His Cys Asn Thr Ala Cys 740	745	750
Leu Thr Asn Ser Ile His Cys Pro Glu Glu Ala Ser Val Gly Asn Pro 755	760	765
Glu Gly Ala Phe Met Lys Met Leu Gln Ala Arg Lys Gln His Met Ser 770	775	780
Thr Gln Leu Thr Ile Glu Ser Glu Ala Pro Ser Asp Ser Ser Gly Ile 785	790	795
Asn Leu Ser Gly Phe Gly Gly Asp Gln Leu Glu Ile Gln Leu Thr Glu 805	810	815
Gln Leu Arg Ser Leu Ile Pro Asn Glu Asp Val Arg Lys Phe Met Ser 820	825	830
His Val Ile Arg Thr Leu Lys Met Glu Cys Ser Glu Thr His Val Gln 835	840	845
Gly Ser Cys Ala Lys Leu Met Ser Arg Thr Gly Leu Leu Met Lys Leu 850	855	860
Leu Ser Glu Gln Gln Glu Ala Lys Ala Leu Asn Val Glu Trp Asp Thr 865	870	875
Asp Gln Gln Lys Thr Asn Tyr Ile Asn Glu Asn Met Glu Gln Asn Glu 885	890	895
Gln Lys Glu Gln Lys Ser Ser Glu Leu Met Lys Glu Val Pro Gly Asp 900	905	910
Asp Tyr Lys Asn Lys Leu Ile Phe Ala Ile Ser Val Thr Val Ile Leu 915	920	925
Ile Ile Leu Ile Ile Ile Phe Cys Leu Ile Glu Val Asn Ser His Lys 930	935	940
Arg Ala Ser Glu Lys Tyr Lys Asp Asn Pro Ser Ile Ser Gly Ala 945	950	955

&lt;210&gt; 109

&lt;211&gt; 1331

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 109

```

gttcttttct tttccatgat atcattatat ggacagttaa ggggtggtctc atggattata 60
accatttggg tatttggttc actaacaatt ttcttactgg ccagagttct tgggtggagaa 120
gttgcatatg gccaaagtcct tggagttata ggatattcat tacttctctc cattgtaata 180
gcccctgtac ttttgggtgt tggatcattt gaagtgggtg ctacacttat aaaactgttt 240
gggtgtgtttt gggctgccta cagtgtgtgt tcattgttag tgggtgaaga attcaagacc 300
aaaaagcctc ttctgattta tccaatcttt ttattataca tttatttttt gtcgttatat 360
actggtgtgt gatccaagtt atacatgaat agaaaaagat ggtgttaaatt ttgtgtgtag 420
gctgggaatt cttgctgaag gaattggaga aaacctgttg ctgcaaaatt ttacatgttc 480
cagatggaaa gggaagtcta agcgctttttt aaaacaattt ttttttgtat ttaattaagc 540

```

```

aattgcagtt atctgggatt tttgggtcag aattttaaat tctgtttgat tctccatatt 600
ccagtgaata aaatacaaaa gcattgtgtt ttaagattg tgcgatatt cacctaaaaa 660
cttgtgccaa aagcacctgg attggttaatt atatttcact taaagggtaa atttgacaat 720
atcttgataa tcaaaagtgc aatttttttc ttcaaaatgt tttctccagc atcacagatc 780
ctgcagatat atatttatat ttatacatat atatttatga aataattctt actcacaaaa 840
tatattttctg ataaacatta agatattaaa tctgatgcac aaacttttta atttggccat 900
taatcttttt tatttaaaaa tttaaatttg tttttaaaat tgtatatagt ttttaaaatc 960
tcacacatgc ttcgatactt ccttggttaag aattcttaat aactactaaa actgattttt 1020
aatagttgct gatatatatt tggtttggtt ggggtatactt ttcaaaacca tttttgaatg 1080
tccaaacatc tgatttaaag tttctgttta tctttctgac caaaggagca agagggtataa 1140
tggatatggc attcattaaa atctttacta tgtacaaaaa cagtaatat tacagcatca 1200
gtaaaatatt ttaagtggta cttctaaatc ataaaagttg gggaaagaga cttttaaaat 1260
cttgtggtgt tgaacaatgt tatatgaagt agaaaaaata aaatacttcc cagttgaaaa 1320
aaaaaaaaa a

```

1331

&lt;210&gt; 110

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 110

```

Met Ile Ser Leu Tyr Gly Gln Phe Arg Val Val Ser Trp Ile Ile Thr
  1             5             10             15

Ile Trp Ile Phe Gly Ser Leu Thr Ile Phe Leu Leu Ala Arg Val Leu
          20             25             30

Gly Gly Glu Val Ala Tyr Gly Gln Val Leu Gly Val Ile Gly Tyr Ser
          35             40             45

Leu Leu Pro Leu Ile Val Ile Ala Pro Val Leu Leu Val Val Gly Ser
          50             55             60

Phe Glu Val Val Ser Thr Leu Ile Lys Leu Phe Gly Val Phe Trp Ala
          65             70             75             80

Ala Tyr Ser Ala Ala Ser Leu Leu Val Gly Glu Glu Phe Lys Thr Lys
          85             90             95

Lys Pro Leu Leu Ile Tyr Pro Ile Phe Leu Leu Tyr Ile Tyr Phe Leu
          100            105            110

Ser Leu Tyr Thr Gly Val
          115

```

&lt;210&gt; 111

&lt;211&gt; 2610

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 111

```

aattgaccat ctctgtgtaa ttctgattgt gtaccttgag acatacagag gattttctatt 60
tctctttttt gcctaagaat gtataaattg tgctatttta ttggggagaa attttatttt 120
tttgtcattt ctctgaagtt gacatttgat gagtgatttc tgaattctac cactcctctg 180
gggaaaaaaa tctcaatgga agattgtaca gttaaagtac ttgtttttcc ctcttgaggt 240
atgctatttt taaggtcatt aatttaaaat agaaatattt ctttaaacca ttgggggtaaa 300
atttttttaa atatggtgct ttgatataat tttgagaaaa gtgcctgaat cctaaaacta 360
actgtctata aagttaagtc cgtataacaa atgattatat atataacaaa gtaaaagtaa 420
atagtgtaga atattaaagt tctcttcag ggcaatgggt attgtggggg attaaacaga 480

```

```

agccccctttg ctatgatcaa ctgcaaaagga aagaaactaa atatgggttca gtgataaaca 540
aaaatagcaa agactgatca ggaaaaatgag aaagagctat gcaaatacag atgatcacca 600
ggccagagaa ttttaagtgc taatagcttt actcctgcat attccatcag tagaatgagc 660
tttttctttt agtctaagtg acactttgaa ggtctttgca ttcattacgc ttttatatac 720
tgcttttctt ttctcttctt tttatttcat ccaacacact aagaaatgaa gaagtttatt 780
gatataattgc ccaataaaaat acaaactctgt tgcaacacaa tgcatatatc ttattagcat 840
tcttggttagt tctaaaattc aattcatcca tagacactta ttcccagcct tcaaatggaa 900
agctctcttt atgcaagaga aaaagggtatt taaaagtgc caaatttttag aatgaggaat 960
tgggttatgct gaatttctgt tccaaaatca ctaggtaaaa tttccatata taataatgta 1020
ttttaggaac aagccaaggt ttgtcattaa gacatagtaa cattaaacta atatttaaaa 1080
atagatttag ctatatattaa tcatgagaaa aggatttctg tggccaggac aaaacccacc 1140
ttgatcctaa agagacatta gcagtgccca tgtcagagcc ttctcacatt cttggaataa 1200
agtaaaccac tccaaggaag gtgagggcac caaatggatc attcttcaaa atgaaaggca 1260
gtctcttact ttctcttgag acatttcttc cctatttggg gattttatga ctgctgttct 1320
ggagagccca catgttttgc ttccatgcag gccaaatcct tctcttgggt ttgggcaaga 1380
gaagttaatc cacctaacag cattttgatt agacaagaat atcatctgat cttatccagg 1440
gacaagaaag tggcatgacc aaaggttctc cttatgtctc tttctttaa tgatttecta 1500
attttcagaa gggctctgga tagactagtt tctgataagg agattttgct gtggtgtctg 1560
ttcttccagg ttaaaggcac acaaagcctt ctgtgtgtcca cttgtgcttg tcttctgaat 1620
tcaactgaaac atggcagaat aaggtttaagg gaaaatgaat tttgacttta catagttaa 1680
tgagtaggag ttacagcaaa aaaaaaaaaa aagacctaaa acttttattt aatagtattc 1740
ttcacctcag gaaattcaga ctttagttg ttcaggtcag aaaatgtgga tatatcctgt 1800
aacactgtct tcacctcact caagttaa at gtaacagcaa atactttcag ctttactttc 1860
aaaaggcttc cagaactttc cacatttcat cactttcact tctacccttc tggtaaaaat 1920
taccaagatt tttagtagtt tactgttccc tgggttctct gatttgatcc ttgctaccat 1980
tctgttttagt cctcaaagaa aaaaaatcaa cattttaaaa cgtttcaatt cttactaatg 2040
gttctcatct cagaagaaaa aacaacgaaa tatcttatgt taatctaaaa aaccttcagt 2100
gacctacttg atctcatttt ctaccatttt cctcctcttt ttctgaaata catcaacaca 2160
gagcactttt cctctccttt aatgcacaaa gatggcagga cttttgaatg ttacatttat 2220
ttatcttctt ctagagtgcc tttccttata caccatgtg acttgttcct cccttccttc 2280
tagtctttgt ttatatatat attattatca cagagggcta ggaaagaaaa caccactgc 2340
tgcgccccac actcatccac ctgcctgtta ccacttactt tgttttggtt ttctctgtag 2400
aattcatgac tttttgaaat ataatttttt taatgtgtac atactttatg ctttctctca 2460
ttcatatgta aagtctggaa gacacagact ggtttttttg ttcactgttg atgcttcagt 2520
ccctaaaata tgcatagcat gaattgccac tttttaaatt aataaatctg gaacattggt 2580
aaaattcaaa aaaaaaaaaa aaaaaaaaaa
2610

```

&lt;210&gt; 112

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 112

```

Met Ala Gly Leu Leu Asn Val Thr Phe Ile Tyr Leu Leu Leu Glu Cys
  1             5             10             15

```

```

Leu Ser Leu Tyr Thr His Val Thr Cys Ser Ser Leu Pro Ser Ser Leu
      20             25             30

```

```

Cys Leu Tyr Ile Tyr Tyr Tyr His Arg Gly Leu Gly Lys Lys Thr Pro
      35             40             45

```

```

Thr Ala Ala Pro His Thr His Pro Pro Ala Leu Tyr His Leu Leu Cys
      50             55             60

```

```

Phe Val Phe Leu Cys Arg Ile His Asp Phe Leu Lys Tyr Asn Phe Phe
      65             70             75             80

```

```

Asn Val Tyr Ile Leu Tyr Ala Phe Ser His Ser Tyr Val Lys Ser Gly
      85             90             95

```

Arg His Arg Leu Val Phe Leu Phe Thr Val Asp Ala Ser Val Pro Lys  
 100 105 110

Ile Cys Ile Ala  
 115

<210> 113  
 <211> 2759  
 <212> DNA  
 <213> Homo sapiens

<400> 113  
 tttttttttt tttgaaagac acacgttatt ttattaatat agccatctct ccccaactgcc 60  
 ccagtgtgta aggtgtttgc attgcaacat ggagggggcac caaatgctct gcggggcccta 120  
 gcccgctgcc acaggctagg cctgcctgca gccaaagaagg ctgctcaaac tctagatgcc 180  
 atttggaggc atgaggacct gagcccagag gtggcagtggt cctacccagg gaagtcaaca 240  
 gatcgtgctc caggtcccag ctctgggctg ggccaggact aaatcctggc tcccccttct 300  
 tgggtactaag gggattagtg cttggtttgtc tgtaggggggt cagagtaggg aggggttcag 360  
 gaaggggttc agagtgggct cacaggggac ctctctccct ggctctctgg agtccaggtc 420  
 gtcgagggcg caaagctgca cgccatcctg ggcaagctgg gcccgagcg tgggcgcggt 480  
 gaggacgcgc agctcatgca gccgctccca agagcaagag aaagcgctcg ggccttcacc 540  
 gcagccgcgc gtgggaggca cactggggta gccggggtgc gccatcagct cggctgtcag 600  
 ggtgtggccc gctagggtac cttccaggac ccgcgccagg gcccgggaca cgcggtgagc 660  
 ggacatgtgc cggccgcaag tgctcaggcc cacgaaggcg tctgtccacc gcaggccgtg 720  
 gcgggagaag ggcccacggc ggcccggcg tcgcgtccca cggcgagcg gaaggcacgc 780  
 gcgggggcct ccagccaagt gcagccacc acaccgcgt ccagcggcag tcgcgtaaag 840  
 cgcaccccat aggcctgcag cgcctcgcg aacacctggc acacgcctgg gagcacgtgc 900  
 acgtgctggt gcccgctcgc gtgcgtgggg gccctgccc gcagctccc gaagcagctt 960  
 agttgggcct cgagctctc ccgcacctag agggcgagcg agagacacct tgagcgaccg 1020  
 ggagtagctg ccgaggatac cctcctcgtg cttccgtgtg atggctccag tgtttgaatg 1080  
 cggaagtcat ccaccgccag ctcttaacgg cctcacagta cctccgggc ggagctctg 1140  
 gggctcctgc gagcatcctc ctgtagctgc ggctccgcac ctgaggcaaa tccacgtctc 1200  
 cggccgccac cgctcccg aatcccatct tgccaaggaa gaagccttc gggccgagca 1260  
 gcgatgaggc gccacggcg gccggacca cggggcgccc ctccgacagg ttggcgtgga 1320  
 ggcccgtggg gatgctgtgc ctgcccggca gctccgcgc gctctccgtg gccgcaccgt 1380  
 tgaccagcag ggacacgctg gtcacggccc cggccagaaa ggctccacg atacctcat 1440  
 cgcgtcgcgg gcagtaacca aagtcgtccg aggtgaccac caggcgccc cgggagccgg 1500  
 cagatccggg tcttgtggct aagagtacg tggtcactcg aatcaaaaaga gaggagggg 1560  
 aggaagccgg cggccagaaa cggcagtgcc agcagcgtcc ggagcagccg cagcctctg 1620  
 gaagctccag gcggtctttc tgccgagcct cggctccggc ccccatcctc cccgccccat 1680  
 cggttgttgt ctgggcggat ttaaacagtc aagtaaaatc aagctgggta atcatggcag 1740  
 aaggtggatt tgatccctgt gaatgtgtt gctctcatga acatgcaatg agaagactga 1800  
 tcaatctgtt acggcagtc cagtcctact gcacagacac agagtgtctt cagggaattac 1860  
 cgggaccctc tgggtgataat ggcatacagt ttacaatgat cttggtagcc tggatgggta 1920  
 ttgcattgat cttgttctta ctgagacct ctaatctaag aggatccagc ctacctggaa 1980  
 agccaaccag tcctcataat ggacaagatc caccagctcc tcctgtggac taactttgtg 2040  
 atatgggaag tgaaaatagt taacacctg caccacaaa cgaacgaaga tgaccagagt 2100  
 actcttaacc ccattagaac tgtttttct tttgtatctg caatatggga tggattgtt 2160  
 ttcattgagct tctagaaatt tcacttgcaa gtttattttt gcttctctg tttactgccat 2220  
 tcctattttac agtatatttg agtgaatgat tatattttta aaaagttaca tggggctttt 2280  
 ttggtgtgcc taaacttaca aacattccac tcattctgtt tgtaactgtg attataattt 2340  
 ttgtgataat ttctggcctg attgaaggaa atttgagagg tctgcattta tatattttta 2400  
 atagatttga taggttttta aattgctttt tttcataagg tatttataaa gttatttggg 2460  
 gttgtctggg attgttgaa agaaaattag aaccacgctg tatttacatt taccttggta 2520  
 gtttatttgt ggaatggcag tttctgtagt ttggggact gtggtagctc ttggattgtt 2580  
 ttgcaaatta cagctgaaat ctgtgtcatg gattaaactg gcttatgtg ctagaatagg 2640  
 aagagaaaaa aaatgaaatg gttgtttact aattttatc tccattaaa aatctcta 2700  
 gtttaaaaaa ccttaataaa acatgattga tcaatatgaa aaaaaaaaaa aaaaaaaaaa 2759

<210> 114  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 114

Met Ala Glu Gly Gly Phe Asp Pro Cys Glu Cys Val Cys Ser His Glu  
 1 5 10 15  
 His Ala Met Arg Arg Leu Ile Asn Leu Leu Arg Gln Ser Gln Ser Tyr  
 20 25 30  
 Cys Thr Asp Thr Glu Cys Leu Gln Glu Leu Pro Gly Pro Ser Gly Asp  
 35 40 45  
 Asn Gly Ile Ser Val Thr Met Ile Leu Val Ala Trp Met Val Ile Ala  
 50 55 60  
 Leu Ile Leu Phe Leu Leu Arg Pro Pro Asn Leu Arg Gly Ser Ser Leu  
 65 70 75 80  
 Pro Gly Lys Pro Thr Ser Pro His Asn Gly Gln Asp Pro Pro Ala Pro  
 85 90 95  
 Pro Val Asp

<210> 115  
 <211> 1404  
 <212> DNA  
 <213> Homo sapiens

<400> 115

aatcggggacg ggacgaatta ttggttgggg gaaacccacg aggggacgcg gccgaggagg 60  
 gtgcgtgtcc acccgggggc gtgggagtga ggtaccagat tcagcccatt tggccccgac 120  
 gcctctgttc tcggaatccg ggtgctgcgg attgaggtcc cggttcctaa cggtgggac 180  
 ggtgtcctcg ggatgagatt tggcgtttcc tcggggcctt ggtgggacg gtgtcctcag 240  
 gatgagattt aggggttctc cggggccttc gggatcttca cctaataatcc ggtattattt 300  
 tatgagagga gtggtcttgg ctgtcagaac tggatccctg gggatgattt tgggaattag 360  
 tggagtgatc tctgaagacc tagggctatg atctggagct gctgtggctg aaatttgggg 420  
 cctctgaagt ggcagtgaga ttgaggtcca gagagcctga gatcttgagg gctgacattt 480  
 ggagagatgg ggtcgagggt tgtcttttgg ccttgactgc tttgggcctt tctcactctc 540  
 attcccggga tgctttgcca gaatctctgc tggattggcc gtaaccctgt ccccgagcgg 600  
 gctcacaggg tctgaaggcc acgcatgagg caaaggtaaa gttctgagcc acccggtgcc 660  
 tccttcccag gactgcaaga tggaggaagg cgggaacctt ggaggcctga ttaagatggg 720  
 ccatctactg gtcttgtcag gtgcctgggg catgcaaag tgggtgacct tcgtctcagg 780  
 tagggaccct cagcttggat gtcatgggta cctgggggtg ggatggaaat aagaggggaa 840  
 ccgggaagtg ccctaacc cctgtgggtc ccataacctg caggcttctc gcttttccga 900  
 agccttcccc gacatacctt cggactagt cagagcaaac tcttccccct ctacttccac 960  
 atctccatgg gctgtgcctt catcaacctc tgcattcttg cttcacagca tgcttgggct 1020  
 cagctcacat tctgggaggc cagccagctt tacctgctgt tcctgagcct tacgctggcc 1080  
 actgtcaacg cccgctggct ggaacccgc accacagctg ccatgtgggc cctgcaaacc 1140  
 gtggagaagg agcgaggcct ggggtggggag gtaccaggca gccaccaggg tcccgatccc 1200  
 taccgcccag tcgagagaaa ggacccaag tacagtgtc tccgccagaa tttcttccgc 1260  
 taccatgggc tgtcctctct ttgcaatctg ggcgtgcctc tgagcaatgg gctctgtctc 1320  
 gctggccttg ccctggaaat aaggagcctc tagcatgggc cctgcatgct aataaatgct 1380  
 tcttcagaaa aaaaaaaaaa aaaa 1404

<210> 116  
 <211> 184  
 <212> PRT  
 <213> Homo sapiens

<400> 116

```

Met Ser Trp Val Pro Gly Val Gly Met Glu Ile Arg Gly Glu Pro Gly
  1             5             10             15

Ser Ala Leu Thr Pro Leu Trp Ser Pro Tyr Pro Ala Gly Phe Leu Leu
      20             25             30

Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys Leu
      35             40             45

Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys Ala Phe Ile Asn Leu
      50             55             60

Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp Glu
      65             70             75             80

Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr Val
      85             90             95

Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala Leu
      100            105            110

Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly Ser
      115            120            125

His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys
      130            135            140

Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser Ser
      145            150            155            160

Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala Gly
      165            170            175

Leu Ala Leu Glu Ile Arg Ser Leu
      180

```

<210> 117  
 <211> 1801  
 <212> DNA  
 <213> Homo sapiens

<400> 117

```

tgaagaagggt gtttactttt ttgaaatta ccttgagaca tttcaaactg tgcagaagat 60
atatgcacaa aagcaaagt cttgcagttt gctatagcca cttatacatc atctggctct 120
tgaatagctt taattcagct gttgaatctc acttgaattt gagcaaaacc ttcattctta 180
tatgtatctg gacaaattac ttcaattgct tgacagtaat gaccaatcaa tttatttaaa 240
atagtatcat ttagtaggac agtggttttc tctggtttga gcaacgaatt caaccagtcc 300
tctgggttga tcatcatcat catcatcatt tggttatcag ttcttgagtt atttttacca 360
gggagtttta tacctttaga caactathtt gaattatctc aggaatgtca tatatctctg 420
cctctttaga gtcagtcact ggcactttgt ctgtttggtg acatcatggt tccctgactg 480
ttcttcatct ttgtagttat acattgatat ctgtgcattg aatatgtagg tatttataaa 540
cagtctttgc aatctggctt tgtctgtgat tgtccttgta tagtaggtct gtccagaaat 600
tgtaagcata ctgtcttttt tggctcttaa gcccgtaac gctacagccc gtgtagtgcc 660

```



```

aaatggtgcc ctaagcccag gttccctgca gtccactctg tgatttggtt gttgactgct 720
gtgagcccca cccccattct ttgtttctaa tttacaccta gcaggctaac cctgctggca 780
cctgcagtgc ttccaggggg aaaggacccat agtgtgcccc tgtgaagagt ctcagaatgg 840
tgcggaaggt gaatgcccac ctcccgtctt cttttccac ttagaaact gattccagag 900
aaattctcca agtgcggtgc tatgtgggct tgcgggagag gtgttatgat caaacagAAC 960
cattctcttt accctctgtt catgggtttt cttggctctg tggccagtg agttgtcaca 1020
gcttcactcc caatttctgg gatattcagg gcaataatct tgccactggg tatttgctag 1080
ttgaaattat gtggtaggga gagaagccag taagcttcac ttctccgttt ggctgatgtc 1140
actctcgaat tctgtacttt catacggatt gtaataggga gggctctaaa ggaagcttca 1200
gttttggtat ttttagagctt cttctaagta caattgttga atcaagaggt aaagatggta 1260
tggtataact ggaaatacgc tgagattaaa aaggagataa attagcccca ttgggacagt 1320
gctattggga atgtgaattg ataccacttt cctggagtct agtttagtat ttattttata 1380
tgtaatgcct gaaaagatgt gtgtctcctt tgactcaata cttataggaa tttacacaaa 1440
gggtataatc aaagattata gaactgttat actggaaaaa cacgaaatat tctaattatg 1500
aattaattgg ggattgggta aataaactat ggtttgatat gctctaaaaa taatgttaca 1560
gaaaaaagtg tactgatatg gcaaaatgta tgacttatag ttaaaaaagc aggttagatg 1620
ttgatagata cagtatgata gaaaaagatc aggaaggat atgctgacat ttaaactctg 1680
atatttatga gtgtttttt tatttcaatc tttgtacat catgtatttt ctagaaattg 1740
tattactatc tttgtaataa agtaaattat ttttaaggga ctaaaaaaaa aaaaaaaaaa 1800
a
1801

```

&lt;210&gt; 118

&lt;211&gt; 86

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 118

```

Met Val Arg Lys Val Asn Ala His Leu Pro Leu Ser Phe Pro Thr Val
 1             5             10             15
Glu Thr Asp Ser Arg Glu Ile Leu Gln Val Arg Cys Tyr Val Gly Leu
          20             25             30
Arg Glu Arg Cys Tyr Asp Gln Thr Glu Pro Phe Ser Leu Pro Ser Val
          35             40             45
His Gly Phe Ser Trp Leu Cys Gly Pro Val Ser Cys His Ser Phe Thr
          50             55             60
Pro Asn Phe Trp Asp Ile Gln Gly Asn Asn Leu Ala Thr Gly Tyr Leu
          65             70             75             80
Leu Val Glu Ile Met Trp
          85

```

&lt;210&gt; 119

&lt;211&gt; 29

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (2)

&lt;223&gt; biotinylated phosphoramidite residue

&lt;400&gt; 119

ancgggagcc tcctgaccat ctcctcttc

29

<210> 120

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 120

cncacagaaa attcaataag accctcgct

29

<210> 121

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 121

cncagctctt cgtagggaag ttctgactt

29

<210> 122

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 122

antcctgcac accagccagt aacgccacc

29

<210> 123

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 123  
gnggctggaa agatgtgtgg ggatcaaga

29

<210> 124  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 124  
anatgggtct aagccacaca acagggtga

29

<210> 125  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 125  
ancggcaggg aacttacagg gacagagct

29

<210> 126  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 126  
gngttttcgg tgctgatggt gtagaggat

29

<210> 127  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 127  
cnagaacaca tagggatgcg agagcaagc 29

<210> 128  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 128  
anactgaaaa ctgagtatgt gcgagtgtgta 29

<210> 129  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 129  
gntatccatt tcctcttctt catctgagt 29

<210> 130  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 130  
tncttgaggc aatggttgaa gtccggcgg 29

<210> 131  
<211> 29

<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> oligonucleotide  
  
<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 131  
tntctgtgctg tgtccttctc tatccgaac

29

<210> 132  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 132  
gngcatctca ctggatgtca tcatcatca

29

<210> 133  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 133  
tngtccatgt gaagggcatg ggccagttg

29

<210> 134  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 134

gngcactgta ttgagctgat tgctgaagc 29

<210> 135  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 135  
cncagaagca gaagaatgac aggcaacac 29

<210> 136  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 136  
anacattctg agtagttgca tgatttccc 29

<210> 137  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 137  
gnccagaaag ttgaggacat gctgggcag 29

<210> 138  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature

<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 138  
angggaacaa gacaactgga gaagggtca 29

<210> 139  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 139  
tngtctccca ggtagacaga gggcttcag 29

<210> 140  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 140  
anccatctac atgtgcattg acaagctta 29

<210> 141  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 141  
tngtgataga tcctttcgta acaccaagt 29

<210> 142  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 142  
angaccagat ctcacccagc acatcaaac 29

<210> 143  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 143  
tntttggggc aagatggctg ttaagcagt 29

<210> 144  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 144  
tngggttggtc cgggcagggc attcttgtc 29

<210> 145  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 145  
tnacacgctc tgtgctagga cttttatat 29

<210> 146  
<211> 29



<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> oligonucleotide  
  
<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 146  
cnggatgtgt gatattggag cttgctgtt

29

<210> 147  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 147  
ancatcaaag gtgcccaaat aagttccca

29

<210> 148  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 148  
anatcactgc atttggtctg gaacctgac

29

<210> 149  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 149

gntgacttca atctcctcac cttccaccg

29

<210> 150

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 150

gnagtgccac ctatgactac caaattctc

29

<210> 151

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 151

gngggatgag gcaatgaaca caatgaaag

29

<210> 152

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 152

cnaaactggt gtttttaccg tatccttca

29

<210> 153

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 153  
tngattctgc cgaatccgaa agtgctctc 29

<210> 154  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 154  
angttgatgg gctcaacaca gggcagagg 29

<210> 155  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 155  
anggatgccca tctctcaccc actctgtac 29

<210> 156  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 156  
anaccaccac ctcgacaggc attccttaa 29

<210> 157  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 157

cncctgaggg tagaaggccg ctcaggttt

29

<210> 158

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 158

tngagtttagc agagcaagaa gcaaggagg

29

<210> 159

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 159

tttgcatgta tagttctctg cagtagcat

29

<210> 160

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 160

anctgccatg tcaaagagga gccagatga

29

<210> 161

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 161  
tnaggcttgt gcacttgctg agcttccag 29

<210> 162  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 162  
cnttcgagca ctaagaacgg gacacggta 29

<210> 163  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 163  
angagaagtt ctgtgcgtgg gtctggtcg 29

<210> 164  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 164  
angtcgttct gcaccaggcc tctgtagcg 29

<210> 165  
<211> 29  
<212> DNA

<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 165  
gntcatctcc agcaccatct ccatcaatg 29

<210> 166  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<400> 166  
actgtctttg aatggtattg 20

<210> 167  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 167  
angttcacat atgatacaag gctctttcc 29

<210> 168  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 168  
cnagtagaca gcacaggtag tcggcttga 29

<210> 169  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 169  
gngaatgcaa tatgaagaaa acaggtcag 29

<210> 170  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 170  
anatcaaggt gattaggctc ttccatgca 29

<210> 171  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 171  
tntacattca atgcctttgc ttctgctg 29

<210> 172  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 172  
antccatgag accaccctaa actgtccat 29

<210> 173  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 173  
gngaggaaaa gtgctctgtg ttgatgtat

29

<210> 174  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 174  
antccacctt ctgccatgat taccagct

29

<210> 175  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue

<400> 175  
anccaagatg cagaggttga tgaaggcac

29

<210> 176  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
<221> misc\_feature  
<222> (2)  
<223> biotinylated phosphoramidite residue



<400> 176  
tntaatgcct gaaaagatgt gtgtctcct

29

<210> 177  
<211> 388  
<212> PRT  
<213> Homo sapiens

<400> 177  
Met His Leu Tyr Lys Thr Asn Lys Met Thr Ser Leu Lys Glu Asp Val  
1 5 10 15  
Arg Arg Ser Ala Met Leu Cys Ile Leu Thr Val Pro Ala Ala Met Thr  
20 25 30  
Ser His Asp Leu Met Lys Phe Val Ala Pro Phe Asn Glu Val Ile Glu  
35 40 45  
Gln Met Lys Ile Ile Arg Asp Ser Thr Pro Asn Gln Tyr Met Val Leu  
50 55 60  
Ile Lys Phe Arg Ala Gln Ala Asp Ala Asp Ser Phe Tyr Met Thr Cys  
65 70 75 80  
Asn Gly Arg Gln Phe Asn Ser Ile Glu Asp Asp Val Cys Gln Leu Val  
85 90 95  
Tyr Val Glu Arg Ala Glu Val Leu Lys Ser Glu Asp Gly Ala Ser Leu  
100 105 110  
Pro Val Met Asp Leu Thr Glu Leu Pro Lys Cys Thr Val Cys Leu Glu  
115 120 125  
Arg Met Asp Glu Ser Val Asn Gly Ile Leu Thr Thr Leu Cys Asn His  
130 135 140  
Ser Phe His Ser Gln Cys Leu Gln Arg Trp Asp Asp Thr Thr Cys Pro  
145 150 155 160  
Val Cys Arg Tyr Cys Gln Thr Pro Glu Pro Val Glu Glu Asn Lys Cys  
165 170 175  
Phe Glu Cys Gly Val Gln Glu Asn Leu Trp Ile Cys Leu Ile Cys Gly  
180 185 190  
His Ile Gly Cys Gly Arg Tyr Val Ser Arg His Ala Tyr Lys His Phe  
195 200 205  
Glu Glu Thr Gln His Thr Tyr Ala Met Gln Leu Thr Asn His Arg Val  
210 215 220  
Trp Asp Tyr Ala Gly Asp Asn Tyr Val His Arg Leu Val Ala Ser Lys  
225 230 235 240  
Thr Asp Gly Lys Ile Val Gln Tyr Glu Cys Glu Gly Asp Thr Cys Gln  
245 250 255  
Glu Glu Lys Ile Asp Ala Leu Gln Leu Glu Tyr Ser Tyr Leu Leu Thr  
260 265 270

Ser Gln Leu Glu Ser Gln Arg Ile Tyr Trp Glu Asn Lys Ile Val Arg  
 275 280 285  
 Ile Glu Lys Asp Thr Ala Glu Glu Ile Asn Asn Met Lys Thr Lys Phe  
 290 295 300  
 Lys Glu Thr Ile Glu Lys Cys Asp Asn Leu Glu His Lys Leu Asn Asp  
 305 310 315 320  
 Leu Leu Lys Glu Lys Gln Ser Val Glu Arg Lys Cys Thr Gln Leu Asn  
 325 330 335  
 Thr Lys Val Ala Lys Leu Thr Asn Glu Leu Lys Glu Glu Gln Glu Met  
 340 345 350  
 Asn Lys Cys Leu Arg Ala Asn Gln Val Leu Leu Gln Asn Lys Leu Lys  
 355 360 365  
 Glu Glu Glu Arg Val Leu Lys Glu Thr Cys Asp Gln Lys Asp Leu Gln  
 370 375 380  
 Ile Thr Glu Ile  
 385

&lt;210&gt; 178

&lt;211&gt; 171

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 178

Met Met Met Gln Cys Val Ser Arg Met Leu Ala His Pro Leu His Val  
 1 5 10 15  
 Ile Ser Met Arg Cys Met Val Gln Phe Val Gly Arg Glu Ala Lys Tyr  
 20 25 30  
 Ser Gly Val Leu Ser Ser Ile Gly Lys Ile Phe Lys Glu Glu Gly Leu  
 35 40 45  
 Leu Gly Phe Phe Val Gly Leu Ile Pro His Leu Leu Gly Asp Val Val  
 50 55 60  
 Phe Leu Trp Gly Cys Asn Leu Leu Ala His Phe Ile Asn Ala Tyr Leu  
 65 70 75 80  
 Val Asp Asp Ser Phe Ser Gln Ala Leu Ala Ile Arg Ser Tyr Thr Lys  
 85 90 95  
 Phe Val Met Gly Ile Ala Val Ser Met Leu Thr Tyr Pro Phe Leu Leu  
 100 105 110  
 Val Gly Asp Leu Met Ala Val Asn Asn Cys Gly Leu Gln Ala Gly Leu  
 115 120 125  
 Pro Pro Tyr Ser Pro Val Phe Lys Ser Trp Ile His Cys Trp Lys Tyr  
 130 135 140  
 Leu Ser Val Gln Gly Gln Leu Phe Arg Gly Ser Ser Leu Leu Phe Arg

145                      150                      155                      160  
 Arg Val Ser Ser Gly Ser Cys Phe Ala Leu Glu  
                                  165                      170  
  
 <210> 179  
 <211> 142  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 179  
 Met His Gln Leu Leu Gln Leu Gln Arg Gln Glu Pro Cys Arg Leu Leu  
   1                                  5                                  10                                  15  
 Ser Pro Ser Pro Gln Pro Gly Leu His His Leu Cys Phe Gln Gln Ile  
                                   20                                  25                                  30  
 Glu Leu Leu Leu Leu Leu Leu His Leu Gln Trp Gly Leu Gly Leu Leu  
                                   35                                  40                                  45  
 Arg Gln Leu His His Lys Arg Leu Ala Gln Leu Leu Leu His Arg Arg  
                                   50                                  55                                  60  
 Arg Asp His Pro Ile Pro Pro Ile Gln Asp Ile Leu Gly Ile Ala Lys  
                                   65                                  70                                  75                                  80  
 Cys Pro Cys Pro Trp Ala Ile Ile Leu Met Arg Met Ala Ser Ile Ile  
                                   85                                  90                                  95  
 Cys His Ile His Gln Cys Ile Thr Arg Val Leu Asp Arg Leu His Thr  
                                   100                                  105                                  110  
 Arg Asp Pro Ser Ser Leu His Thr Pro Ser Leu Ser Pro His Ser Ser  
                                   115                                  120                                  125  
 Leu Thr Ile His Ser Ser Asn Met Ser Ala Gln Gln Leu Ser  
                                   130                                  135                                  140  
  
 <210> 180  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 180  
 Met Gly Pro Val Ser Ala Gly Ser Gln Gly Cys Gly Thr Cys Ala Val  
   1                                  5                                  10                                  15  
 Lys Leu Ala Pro Thr Trp Arg Ala Ala Ala Ala Thr Cys Phe Leu Gln  
                                   20                                  25                                  30  
 His Leu Leu Pro Cys Ser Val Ser Ser Leu Ser Pro Arg Leu Ala Gln  
                                   35                                  40                                  45  
 Glu Cys Trp Lys Ser Ser Arg Leu Gly Leu Gly Ala Trp Pro Leu Asp  
                                   50                                  55                                  60  
 Ile Pro Arg Ala Ser Pro Val Leu Pro Ser Pro Arg Thr Thr Gly Pro  
                                   65                                  70                                  75                                  80

Leu Ala

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US99/09970

**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(6) :C07H 21/04; C07K 14/705; C12N 15/09, 15/63; C12Q 1/68

US CL :Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1, 24.3; 435/7.2, 69.1; 530/350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

GENEMBL,N-GENSEQ-34, EST, A-GENSEQ35, PIR60, SWISS-PROT37, SPTREMBL19, APS, MEDLINE, CAPLUS, WPIDS, JAPIO, SCISEARCH

Search terms: secreted protein, bn36553, gage 1, gage 6, rgd

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X - Y	Database EST, Accession Number AA242967, HILLIER, L. et al. WashU_Merck EST Project 1997, 06 August 1997.	1-3 ----- 4-7, 9, 11
X - Y	Database EST, Accession Number AA524997, NCI-CGAP <a href="http://www.nci.nlm.nih.gov/ncicgap">http://www.nci.nlm.nih.gov/ncicgap</a> , National cancer Institute, cancer Genome AnDatomy Project (CGAP), Tumor Gene Index. 05 August 1997.	1-3 ----- 4-7, 9, 11
X,P --- Y,P	Database Sptrembl19, Accession Number 060829, STROM, T. M et al. JM27 Protein, Complete CDs (Clone Image 145745 and Image 257878), 01 August 1998.	1-3 ----- 4-7, 9, 11
X,P --- Y,P	Database GenEmbl, Accession Number HSA005894, AJ005894, STROM, T. M. et al. Transcription map in Hp11.23, 15 May 1998.	1-3 ----- 4-7, 9, 11

<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C.	<input type="checkbox"/> See patent family annex.
* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
*A* document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
*B* earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
*L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A* document member of the same patent family
*O* document referring to an oral disclosure, use, exhibition or other means	
*P* document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search 22 JULY 1999	Date of mailing of the international search report 09 SEP 1999
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer NIRMAL S. BASI Telephone No. (703) 308-0196

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US99/09970

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	ROBINSON, A.K. et al. A Gene from the Hyperthermophile <i>Pyrococcus furiosus</i> whose Deduced Product is Homologous to Members of the Prolyl Oligopeptidase Family of Proteases. <i>Gene</i> . 1995, Vol. 152, pages 103-106, see Fig. 1, amino acids 358-365.	9, 11
Y	BERGER, S.L. et al. Guide to Molecular Cloning Techniques. <i>Methods in Enzymology</i> . 1987, Vol. 152, pages 661-673, see entire document.	1-7, 9, 11

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US99/09970

**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
1-11

Remark on Protest

☐  
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US99/09970

## A. CLASSIFICATION OF SUBJECT MATTER:

US CL :

536/23.1, 24.3; 435/7.2, 69.1; 530/350

## BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s)1-11, drawn to polynucleotide comprising SEQ ID NO:1, fragments thereof, expression vector containing said sequence, cell transformed with said vector, polypeptide of SEQ ID NO:2, fragments of the polypeptide of SEQ ID NO:2, process for preparing said polypeptide.

Group II, claim(s)12-13, drawn to polynucleotides comprising SEQ ID NO:3, fragments thereof, polypeptide of SEQ ID NO:4, fragments of the polypeptide of SEQ ID NO:4.

Group III, claim(s)14-15, drawn to polynucleotides comprising SEQ ID NO:5, fragments thereof, polypeptide of SEQ ID NO:6, fragments of the polypeptide of SEQ ID NO:6.

Group IV, claim(s)16-17, drawn to polynucleotides comprising SEQ ID NO:7, fragments thereof, polypeptide of SEQ ID NO:8, fragments of the polypeptide of SEQ ID NO:8.

Group V, claim(s)18-19, drawn to polynucleotides comprising SEQ ID NO:9, fragments thereof, polypeptide of SEQ ID NO:10, fragments of the polypeptide of SEQ ID NO:10.

Group VI, claim(s)20-21, drawn to polynucleotides comprising SEQ ID NO:11, fragments thereof, polypeptide of SEQ ID NO:12, fragments of the polypeptide of SEQ ID NO:12.

Group VII, claim(s)22-23, drawn to polynucleotides comprising SEQ ID NO:13, fragments thereof, polypeptide of SEQ ID NO:14, fragments of the polypeptide of SEQ ID NO:14.

Group VIII, claim(s)24-25, drawn to polynucleotides comprising SEQ ID NO:15, fragments thereof, polypeptide of SEQ ID NO:16, fragments of the polypeptide of SEQ ID NO:16.

Group IX, claim(s)26-27, drawn to polynucleotides comprising SEQ ID NO:17, fragments thereof, polypeptide of SEQ ID NO:18, fragments of the polypeptide of SEQ ID NO:18.

Group X, claim(s)28-29, drawn to polynucleotides comprising SEQ ID NO:19, fragments thereof, polypeptide of SEQ ID NO:20, fragments of the polypeptide of SEQ ID NO:20.

Group XI, claim(s)30-31, drawn to polynucleotides comprising SEQ ID NO:21, fragments thereof, polypeptide of SEQ ID NO:22, fragments of the polypeptide of SEQ ID NO:22.

Group XII, claim(s)32-33, drawn to polynucleotides comprising SEQ ID NO:23, fragments thereof, polypeptide of SEQ ID NO:24, fragments of the polypeptide of SEQ ID NO:24.

Group XIII, claim(s)34-35, drawn to polynucleotides comprising SEQ ID NO:25, fragments thereof, polypeptide of SEQ ID NO:26, fragments of the polypeptide of SEQ ID NO:26.

Group XIV, claim(s)36-37, drawn to polynucleotides comprising SEQ ID NO:27, fragments thereof, polypeptide of SEQ ID NO:28, fragments of the polypeptide of SEQ ID NO:28.

Group XV, claim(s)38-39, drawn to polynucleotides comprising SEQ ID NO:29, fragments thereof, polypeptide of SEQ ID NO:30, fragments of the polypeptide of SEQ ID NO:30.

Group XVI, claim(s)40-41, drawn to polynucleotides comprising SEQ ID NO:31, fragments thereof, polypeptide of SEQ ID NO:32, fragments of the polypeptide of SEQ ID NO:32.

Group XVII, claim(s)42-43, drawn to polynucleotides comprising SEQ ID NO:33, fragments thereof, polypeptide of SEQ ID NO:34, fragments of the polypeptide of SEQ ID NO:34.

Group XVIII, claim(s)44-45, drawn to polynucleotides comprising SEQ ID NO:35, fragments thereof, polypeptide of SEQ ID NO:36, fragments of the polypeptide of SEQ ID NO:36.

Group XIX, claim(s)46-47, drawn to polynucleotides comprising SEQ ID NO:37, fragments thereof, polypeptide of SEQ ID NO:38, fragments of the polypeptide of SEQ ID NO:38.

Group XX, claim(s)48-49, drawn to polynucleotides comprising SEQ ID NO:39, fragments thereof, polypeptide of SEQ ID NO:40, fragments of the polypeptide of SEQ ID NO:40.

Group XXI, claim(s)50-51, drawn to polynucleotides comprising SEQ ID NO:41, fragments thereof, polypeptide of SEQ ID NO:42, fragments of the polypeptide of SEQ ID NO:42.

Group XXII, claim(s)52-53, drawn to polynucleotides comprising SEQ ID NO:43, fragments thereof, polypeptide of SEQ ID NO:44, fragments of the polypeptide of SEQ ID NO:44.

Group XXIII, claim(s)54-55, drawn to polynucleotides comprising SEQ ID NO:45, fragments thereof, polypeptide of SEQ ID NO:46, fragments of the polypeptide of SEQ ID NO:46.

Group XXIV, claim(s)56-57, drawn to polynucleotides comprising SEQ ID NO:47, fragments thereof,



## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US99/09970

polypeptide of SEQ ID NO:48, fragments of the polypeptide of SEQ ID NO:48.

Group XXV, claim(s)58-59, drawn to polynucleotides comprising SEQ ID NO:49, fragments thereof, polypeptide of SEQ ID NO:50, fragments of the polypeptide of SEQ ID NO:50.

Group XXVI, claim(s)60-61, drawn to polynucleotides comprising SEQ ID NO:51, fragments thereof, polypeptide of SEQ ID NO:52, fragments of the polypeptide of SEQ ID NO:52.

Group XXVII, claim(s)62-63, drawn to polynucleotides comprising SEQ ID NO:53, fragments thereof, polypeptide of SEQ ID NO:54, fragments of the polypeptide of SEQ ID NO:54.

Group XXVIII, claim(s)64-65, drawn to polynucleotides comprising SEQ ID NO:55, fragments thereof, polypeptide of SEQ ID NO:56, fragments of the polypeptide of SEQ ID NO:56.

Group XXIX, claim(s)66-67, drawn to polynucleotides comprising SEQ ID NO:57, fragments thereof, polypeptide of SEQ ID NO:58, fragments of the polypeptide of SEQ ID NO:58.

Group XXX, claim(s)68-69, drawn to polynucleotides comprising SEQ ID NO:59, fragments thereof, polypeptide of SEQ ID NO:60, fragments of the polypeptide of SEQ ID NO:60.

Group XXXI, claim(s)70-71, drawn to polynucleotides comprising SEQ ID NO:61, fragments thereof, polypeptide of SEQ ID NO:62, fragments of the polypeptide of SEQ ID NO:62.

Group XXXII, claim(s)72-73, drawn to polynucleotides comprising SEQ ID NO:63, fragments thereof, polypeptide of SEQ ID NO:64, fragments of the polypeptide of SEQ ID NO:64.

Group XXXIII, claim(s)74-75, drawn to polynucleotides comprising SEQ ID NO:65, fragments thereof, polypeptide of SEQ ID NO:66, fragments of the polypeptide of SEQ ID NO:66.

Group XXXIV, claim(s)76-77, drawn to polynucleotides comprising SEQ ID NO:67, fragments thereof, polypeptide of SEQ ID NO:68, fragments of the polypeptide of SEQ ID NO:68.

Group XXXV, claim(s)78-79, drawn to polynucleotides comprising SEQ ID NO:69, fragments thereof, polypeptide of SEQ ID NO:70, fragments of the polypeptide of SEQ ID NO:70.

Group XXXVI, claim(s)80-81, drawn to polynucleotides comprising SEQ ID NO:71, fragments thereof, polypeptide of SEQ ID NO:72, fragments of the polypeptide of SEQ ID NO:72.

Group XXXVII, claim(s)82-83, drawn to polynucleotides comprising SEQ ID NO:73, fragments thereof, polypeptide of SEQ ID NO:74, fragments of the polypeptide of SEQ ID NO:74.

Group XXXVIII, claim(s)84-85, drawn to polynucleotides comprising SEQ ID NO:75, fragments thereof, polypeptide of SEQ ID NO:76, fragments of the polypeptide of SEQ ID NO:76.

Group XXXIX, claim(s)86-87, drawn to polynucleotides comprising SEQ ID NO:77, fragments thereof, polypeptide of SEQ ID NO:78, fragments of the polypeptide of SEQ ID NO:78.

Group XL, claim(s)88-89, drawn to polynucleotides comprising SEQ ID NO:79, fragments thereof, polypeptide of SEQ ID NO:80, fragments of the polypeptide of SEQ ID NO:80.

Group XLI, claim(s)90-91, drawn to polynucleotides comprising SEQ ID NO:81, fragments thereof, polypeptide of SEQ ID NO:82, fragments of the polypeptide of SEQ ID NO:82.

Group XLII, claim(s)92-93, drawn to polynucleotides comprising SEQ ID NO:83, fragments thereof, polypeptide of SEQ ID NO:84, fragments of the polypeptide of SEQ ID NO:84.

Group XLIII, claim(s)94-95, drawn to polynucleotides comprising SEQ ID NO:85, fragments thereof, polypeptide of SEQ ID NO:86, fragments of the polypeptide of SEQ ID NO:86.

Group XLIV, claim(s)96-97, drawn to polynucleotides comprising SEQ ID NO:87, fragments thereof, polypeptide of SEQ ID NO:88, fragments of the polypeptide of SEQ ID NO:88.

Group XLV, claim(s)98-99, drawn to polynucleotides comprising SEQ ID NO:89, fragments thereof, polypeptide of SEQ ID NO:90, fragments of the polypeptide of SEQ ID NO:90.

Group XLVI, claim(s)100-101, drawn to polynucleotides comprising SEQ ID NO:91, fragments thereof, polypeptide of SEQ ID NO:92, fragments of the polypeptide of SEQ ID NO:92.

Group XLVII, claim(s)102-103, drawn to polynucleotides comprising SEQ ID NO:93, fragments thereof, polypeptide of SEQ ID NO:94, fragments of the polypeptide of SEQ ID NO:94.

Group XLVIII, claim(s)104-105, drawn to polynucleotides comprising SEQ ID NO:95, fragments thereof, polypeptide of SEQ ID NO:96, fragments of the polypeptide of SEQ ID NO:96.

Group XLIX, claim(s)106-107, drawn to polynucleotides comprising SEQ ID NO:97, fragments thereof, polypeptide of SEQ ID NO:98, fragments of the polypeptide of SEQ ID NO:98.

Group L, claim(s)108-109, drawn to polynucleotides comprising SEQ ID NO:99, fragments thereof, polypeptide of SEQ ID NO:100, fragments of the polypeptide of SEQ ID NO:100.

Group LI, claim(s)110-111, drawn to polynucleotides comprising SEQ ID NO:101, fragments thereof, polypeptide of SEQ ID NO:102, fragments of the polypeptide of SEQ ID NO:102.

Group LII, claim(s)112-113, drawn to polynucleotides comprising SEQ ID NO:103, fragments thereof, polypeptide of SEQ ID NO:104, fragments of the polypeptide of SEQ ID NO:104.

Group LIII, claim(s)114-115, drawn to polynucleotides comprising SEQ ID NO:105, fragments thereof, polypeptide of SEQ ID NO:106, fragments of the polypeptide of SEQ ID NO:106.

Group LIV, claim(s)116-117, drawn to polynucleotides comprising SEQ ID NO:107, fragments thereof, polypeptide of SEQ ID NO:108, fragments of the polypeptide of SEQ ID NO:108.

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US99/09970

Group LV, claim(s)118-119, drawn to polynucleotides comprising SEQ ID NO:109, fragments thereof, polypeptide of SEQ ID NO:110, fragments of the polypeptide of SEQ ID NO:110.

Group LVI, claim(s)120-121, drawn to polynucleotides comprising SEQ ID NO:111, fragments thereof, polypeptide of SEQ ID NO:112, fragments of the polypeptide of SEQ ID NO:112

Group LVII, claim(s)122-123, drawn to polynucleotides comprising SEQ ID NO:113, fragments thereof, polypeptide of SEQ ID NO:114, fragments of the polypeptide of SEQ ID NO:114.

Group LVIII, claim(s)124-125, drawn to polynucleotides comprising SEQ ID NO:115, fragments thereof, polypeptide of SEQ ID NO:116, fragments of the polypeptide of SEQ ID NO:116.

Group LVIII, claim(s)126-127, drawn to polynucleotides comprising SEQ ID NO:117, fragments thereof, polypeptide of SEQ ID NO:118, fragments of the polypeptide of SEQ ID NO:118.

The inventions listed as Groups I-LVIII do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: The main invention is Group I, which is first product, first method of making the product and first method of using the product. Pursuant to 37 CFR 1.474 (d), these claims are considered by the ISA/US to constitute the main invention and none of the related Groups II-LVIII correspond to the main invention. The products of Groups II-LVIII do not share the same or corresponding special technical feature with Group I because they are drawn to products having materially different structures and functions, each defines a separate invention over the art. Therefore, the claims are not linked by a special technical feature within the meaning of PCT Rule 13.2 so as to form a single inventive concept.